

SEQUENCE LISTING

(1) GENERAL INFORMATION:

5 (i) APPLICANT: ANDREW C. HIATT, JULIAN
K.-C. MA, THOMAS LEHNER

(ii) TITLE OF INVENTION: IMMUNOGLOBULINS CONTAINING PROTECTION
10 PROTEINS IN PLANTS AND THEIR USES

(iii) NUMBER OF SEQUENCES: 19

(iv) CORRESPONDENCE ADDRESS:

15 (A) ADDRESSEE: Lyon & Lyon
(B) STREET: 633 West Fifth Street
Suite 4700
(C) CITY: Los Angeles
(D) STATE: California
20 (E) COUNTRY: U.S.A.
(F) ZIP: 90071

(v) COMPUTER READABLE FORM:

25 (A) MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
storage
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: IBM P.C. DOS 5.0
(D) SOFTWARE: Word Perfect 5.1
30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: TO BE ASSIGNED
(B) FILING DATE:
35 (C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

40 Prior applications total,
including application
described below: 1

45 U.S. Patent Application Serial No. 08/367,395
Filed 12/30/94
Docket No. 210/152

(viii) ATTORNEY/AGENT INFORMATION:

5 (A) NAME: Guise, Jeffrey W.
(B) REGISTRATION NUMBER: 34,613
(C) REFERENCE/DOCKET NUMBER: 212/127

(ix) TELECOMMUNICATION INFORMATION:

10 (A) TELEPHONE: (619) 552-8400
(B) TELEFAX: (619) 552-0159
(C) TELEX: 67-3510

2025 FEB 20 10 23 53

SEQUENCE LISTING

5 (2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 3517 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 DESCRIPTION: Rabbit polyimmunoglobulin receptor

15 (ix) FEATURE:

(A) NAME/KEY: Coding Sequence
 (B) LOCATION: 124....2445

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

GGCCGGGGTT ACGGGCTGGC CAGCAGGCTG TGCCCCCGAG TCCGGTCAGCAGGAGGGGAA 60
 GAAGTGGCCT AAAATCTCTC CCGCATCGGC AGCCCAGGCC TAGTGCCCTA CCAGCCACCA 120
 25 GCC ATG GCT CTC TTC TTG CTC ACC TGC CTG CTG GCT GTC TTT TCA GCG 168
 Met Ala Leu Phe Leu Leu Thr Cys Leu Leu Ala Val Phe Ser Ala
 1 5 10 15
 30 GCC ACG GCA CAA AGC TCC TTA TTG GGT CCC AGC TCC ATA TTT GGT CCC 216
 Ala Thr Ala Gln Ser Ser Leu Leu Gly Pro Ser Ser Ile Phe Gly Pro
 20 25 30
 35 GGG GAG GTG AAT GTT TTG GAA GGC GAC TCG GTG TCC ATC ACA TGC TAC 264
 Gly Glu Val Asn Val Leu Glu Gly Asp Ser Val Ser Ile Thr Cys Tyr
 35 40 45
 40 TAC CCA ACA ACC TCC GTC ACC CGG CAC AGC CGG AAG TTC TGG TGC CGG 312
 Tyr Pro Thr Thr Ser Val Thr Arg His Ser Arg Lys Phe Trp Cys Arg
 50
 GAA GAG GAG AGC GGC CGC TGC GTG ACG CTT GCC TCG ACC GGC TAC ACG 360
 Glu Glu Glu Ser Gly Arg Cys Val Thr Leu Ala Ser Thr Gly Tyr Thr
 65 70 75
 45 TCC CAG GAA TAC TCC GGG AGA GGC AAG CTC ACC GAC TTC CCT GAT AAA 408
 Ser Gln Glu Tyr Ser Gly Arg Gly Lys Leu Thr Asp Phe Pro Asp Lys
 80 85 90 95
 50 GGG GAG TTT GTG GTG ACT GTT GAC CAA CTC ACC CAG AAC GAC TCA GGG 456
 Gly Glu Phe Val Val Thr Val Asp Gln Leu Thr Gln Asn Asp Ser Gly
 100 105 110
 55 AGC TAC AAG TGT GGC GTG GGA GTC AAC GGC CGT GGC CTG GAC TTC GGT 504
 Ser Tyr Lys Cys Gly Val Gly Val Asn Gly Arg Gly Leu Asp Phe Gly
 115 120 125
 GTC AAC GTG CTG GTC AGC CAG AAG CCA GAG CCT GAT GAC GTT GTT TAC 552
 Val Asn Val Leu Val Ser Gln Lys Pro Glu Pro Asp Asp Val Val Tyr
 130 135 140
 60 AAA CAA TAT GAG AGT TAT ACA GTA ACC ATC ACC TGC CCT TTC ACA TAT 600
 Lys Gln Tyr Glu Ser Tyr Thr Val Thr Ile Thr Cys Pro Phe Thr Tyr
 145 150 155
 65 GCG ACT AGG CAA CTA AAG AAG TCC TTT TAC AAG GTG GAA GAC GGG GAA 648

	Ala	Thr	Arg	Gln	Leu	Lys	Lys	Ser	Phe	Tyr	Lys	Val	Glu	Asp	Gly	Glu	
	160					165					170					175	
5	CTT	GTA	CTC	ATC	ATT	GAT	TCC	AGC	AGT	AAG	GAG	GCA	AAG	GAC	CCC	AGG	696
	Leu	Val	Leu	Ile	Ile	Asp	Ser	Ser	Ser	Lys	Glu	Ala	Lys	Asp	Pro	Arg	
					180					185					190		
10	TAT	AAG	GGC	AGA	ATA	ACG	TTG	CAG	ATC	CAA	AGT	ACC	ACA	GCA	AAA	GAA	744
	Tyr	Lys	Gly	Arg	Ile	Thr	Leu	Gln	Ile	Gln	Ser	Thr	Thr	Ala	Lys	Glu	
				195					200					205			
15	TTC	ACA	GTC	ACC	ATC	AAG	CAT	TTG	CAG	CTC	AAT	GAT	GCT	GGG	CAG	TAT	792
	Phe	Thr	Val	Thr	Ile	Lys	His	Leu	Gln	Leu	Asn	Asp	Ala	Gly	Gln	Tyr	
			210					215					220				
20	GTC	TGC	CAG	AGT	GGA	AGC	GAC	CCC	ACT	GCT	GAA	GAA	CAG	AAC	GTT	GAC	840
	Val	Cys	Gln	Ser	Gly	Ser	Asp	Pro	Thr	Ala	Glu	Glu	Gln	Asn	Val	Asp	
		225					230				235						
25	CTC	CGA	CTG	CTA	ACT	CCT	GGT	CTG	CTC	TAT	GGA	AAC	CTG	GGG	GGC	TCG	888
	Leu	Arg	Leu	Leu	Thr	Pro	Gly	Leu	Leu	Tyr	Gly	Asn	Leu	Gly	Gly	Ser	
						245					250					255	
30	GTG	ACC	TTT	GAA	TGT	GCC	CTG	GAC	TCT	GAA	GAC	GCA	AAC	GCG	GTA	GCA	936
	Val	Thr	Phe	Glu	Cys	Ala	Leu	Asp	Ser	Glu	Asp	Ala	Asn	Ala	Val	Ala	
					260					265					270		
35	TCC	TTG	CGC	CAG	GTT	AGG	GGT	GGC	AAT	GTG	GTC	ATT	GAC	AGC	CAG	GGG	984
	Ser	Leu	Arg	Gln	Val	Arg	Gly	Gly	Asn	Val	Val	Ile	Asp	Ser	Gln	Gly	
				275					280					285			
40	ACA	ATA	GAT	CCA	GCC	TTC	GAG	GGC	AGG	ATC	CTG	TTC	ACC	AAG	GCT	GAG	1032
	Thr	Ile	Asp	Pro	Ala	Phe	Glu	Gly	Arg	Ile	Leu	Phe	Thr	Lys	Ala	Glu	
			290					295					300				
45	AAC	GGC	CAC	TTC	AGT	GTA	GTG	ATC	GCA	GGC	CTG	AGG	AAG	GAA	GAC	ACA	1080
	Asn	Gly	His	Phe	Ser	Val	Val	Ile	Ala	Gly	Leu	Arg	Lys	Glu	Asp	Thr	
		305					310					315					
50	GGG	AAC	TAT	CTG	TGC	GGA	GTC	CAG	TCC	AAT	GGT	CAG	TCT	GGG	GAT	GGG	1128
	Gly	Asn	Tyr	Leu	Cys	Gly	Val	Gln	Ser	Asn	Gly	Gln	Ser	Gly	Asp	Gly	
		320				325					330					335	
55	CCC	ACC	CAG	CTT	CGG	CAA	CTC	TTC	GTC	AAT	GAA	GAG	ATC	GAC	GTG	TCC	1176
	Pro	Thr	Gln	Leu	Arg	Gln	Leu	Phe	Val	Asn	Glu	Glu	Ile	Asp	Val	Ser	
					340					345					350		
60	CGC	AGC	CCC	CCT	GTG	TTG	AAG	GGC	TTT	CCA	GGA	GGC	TCC	GTG	ACC	ATA	1224
	Arg	Ser	Pro	Pro	Val	Leu	Lys	Gly	Phe	Pro	Gly	Gly	Ser	Val	Thr	Ile	
				355					360					365			
65	CGC	TGC	CCC	TAC	AAC	CCG	AAG	AGA	AGC	GAC	AGC	CAC	CTG	CAG	CTG	TAT	1272
	Arg	Cys	Pro	Tyr	Asn	Pro	Lys	Arg	Ser	Asp	Ser	His	Leu	Gln	Leu	Tyr	
			370					375					380				
70	CTC	TGG	GAA	GGG	AGT	CAA	ACC	CGC	CAT	CTG	CTG	GTG	GAC	AGC	GGC	GAG	1320
	Leu	Trp	Glu	Gly	Ser	Gln	Thr	Arg	His	Leu	Leu	Val	Asp	Ser	Gly	Glu	
		385					390					395					
75	GGG	CTG	GTT	CAG	AAA	GAC	TAC	ACA	GGC	AGG	CTG	GCC	CTG	TTC	GAA	GAG	1368
	Gly	Leu	Val	Gln	Lys	Asp	Tyr	Thr	Gly	Arg	Leu	Ala	Leu	Phe	Glu	Glu	
		400				405					410					415	
80	CCT	GGC	AAT	GGC	ACC	TTC	TCA	GTC	GTC	CTC	AAC	CAG	CTC	ACT	GCC	GAG	1416
	Pro	Gly	Asn	Gly	Thr	Phe	Ser	Val	Val	Leu	Asn	Gln	Leu	Thr	Ala	Glu	
					420					425					430		

T03T0T 43T23650

	GAT Asp	GAA Glu	GGC Gly	TTC Phe 435	TAC Tyr	TGG Trp	TGT Cys	GTC Val	AGC Ser 440	GAT Asp	GAC Asp	GAT Asp	GAG Glu	TCC Ser 445	CTG Leu	ACG Thr	1464
5	ACT Thr	TCG Ser	GTG Val 450	AAG Lys	CTC Leu	CAG Gln	ATC Ile	GTT Val 455	GAC Asp	GGA Gly	GAA Glu	CCA Pro	AGC Ser 460	CCC Pro	ACG Thr	ATC Ile	1512
10	GAC Asp	AAG Lys 465	TTC Phe	ACT Thr	GCT Ala	GTG Val	CAG Gln 470	GGA Gly	GAG Glu	CCT Pro	GTT Val	GAG Glu 475	ATC Ile	ACC Thr	TGC Cys	CAC His	1560
15	TTC Phe 480	CCA Pro	TGC Cys	AAA Lys	TAC Tyr	TTC Phe 485	TCC Ser	TCC Ser	GAG Glu	AAG Lys	TAC Tyr 490	TGG Trp	TGC Cys	AAG Lys	TGG Trp	AAT Asn 495	1608
20	GAC Asp	CAT His	GGC Gly	TGC Cys 500	GAG Glu	GAC Asp	CTG Leu	CCC Pro	ACT Thr	AAG Lys 505	CTC Leu	AGC Ser	TCC Ser	AGC Ser	GGC Gly 510	GAC Asp	1656
	CTT Leu	GTG Val	AAA Lys 515	TGC Cys	AAC Asn	AAC Asn	AAC Asn	CTG Leu 520	GTC Val	CTC Leu	ACC Thr	CTG Leu	ACC Thr 525	TTG Leu	GAC Asp	TCG Ser	1704
25	GTC Val	AGC Ser	GAA Glu 530	GAT Asp	GAC Asp	GAG Glu	GGC Gly	TGG Trp 535	TAC Tyr	TGG Trp	TGT Cys	GGC Gly	GCG Ala 540	AAA Lys	GAC Asp	GGG Gly	1752
30	CAC His 545	GAG Glu	TTT Phe	GAA Glu	GAG Glu	GTT Val	GCG Ala 550	GCC Ala	GTC Val	AGG Arg	GTG Val	GAG Glu 555	CTG Leu	ACA Thr	GAG Glu	CCA Pro	1800
35	GCC Ala 560	AAG Lys	GTA Val	GCT Ala	GTC Val	GAG Glu 565	CCA Pro	GCC Ala	AAG Lys	GTA Val	CCT Pro 570	GTC Val	GAC Asp	CCA Pro	GCC Ala	AAG Lys 575	1848
	GCA Ala	GCC Ala	CCC Pro	GCG Ala	CCT Pro 580	GCT Ala	GAG Glu	GAG Glu	AAG Lys	GCC Ala 585	AAG Lys	GCG Ala	CGG Arg	TGC Cys	CCA Pro 590	GTG Val	1896
40	CCC Pro	AGG Arg	AGA Arg	AGG Arg 595	CAG Gln	TGG Trp	TAC Tyr	CCA Pro	TTG Leu 600	TCA Ser	AGG Arg	AAG Lys	CTG Leu 605	AGA Arg	ACA Thr	AGT Ser	1944
45	TGT Cys	CCA Pro	GAA Glu 610	CCT Pro	CGG Arg	CTC Leu	CTT Leu	GCG Ala 615	GAG Glu	GAG Glu	GTA Val	GCA Ala	GTG Val 620	CAG Gln	AGT Ser	GCG Ala	1992
50	GAA Glu 625	GAC Asp	CCA Pro	GCC Ala	AGT Ser	GGG Gly	AGC Ser 630	AGA Arg	GCG Ala	TCT Ser	GTG Val	GAT Asp 635	GCC Ala	AGC Ser	AGT Ser	GCT Ala	2040
55	TCG Ser 640	GGA Gly	CAA Gln	AGC Ser	GGG Gly	AGT Ser 645	GCC Ala	AAA Lys	GTA Val	CTG Leu	ATC Ile 650	TCC Ser	ACC Thr	CTG Leu	GTG Val	CCC Pro 655	2088
	TTG Leu	GGG Gly	CTG Leu	GTG Val 660	CTG Leu	GCA Ala	GCG Ala	GGG Gly	GCC Ala	ATG Met 665	GCC Ala	GTG Val	GCC Ala	ATA Ile	GCC Ala 670	AGA Arg	2136
60	GCC Ala	CGG Arg	CAC His	AGG Arg 675	AGG Arg	AAC Asn	GTG Val	GAC Asp	CGA Arg 680	GTT Val	TCC Ser	ATC Ile	GGA Gly	AGC Ser 685	TAC Tyr	AGG Arg	2184
65	ACA Thr	GAC Asp	ATT Ile	AGC Ser	ATG Met	TCA Ser	GAC Asp	TTG Leu	GAG Glu	AAC Asn	TCC Ser	AGG Arg	GAG Glu	TTC Phe	GGA Gly	GCC Ala	2232

	690	695	700	
5	ATT GAC AAC CCA AGC GCC TGC CCC GAT GCC CGG GAG ACG GCC CTC GGA Ile Asp Asn Pro Ser Ala Cys Pro Asp Ala Arg Glu Thr Ala Leu Gly 705 710 715			2280
10	GGA AAG GAT GAG TTA GCG ACG GCC ACC GAG AGC ACC GTG GAG ATT GAG Gly Lys Asp Glu Leu Ala Thr Ala Thr Glu Ser Thr Val Glu Ile Glu 720 725 730 735			2328
	GAG CCC AAG AAG GCA AAA CGG TCA TCC AAG GAA GAA GCC GAC CTG GCC Glu Pro Lys Lys Ala Lys Arg Ser Ser Lys Glu Glu Ala Asp Leu Ala 740 745 750			2376
15	TAC TCA GCT TTC CTG CTC CAA TCC AAC ACC ATA GCT GCT GAG CAC CAA Tyr Ser Ala Phe Leu Leu Gln Ser Asn Thr Ile Ala Ala Glu His Gln 755 760 765			2424
20	GAT GGC CCC AAG GAG GCC TAG GCACAGCCGG CCACCGCCGC CGCCGCCACC GCCGC Asp Gly Pro Lys Glu Ala 770			2480
	CGCCGCCGCC ACCTGTGAAA ATCACCTTCC AGAATCACGT TGATCCTCGG GGTCCCCAGA			2540
25	GCCGGGGGCT CAACCGCCCT GCACCCCCCA TGTCCCCACC ACCTAAACTT CCCTACCTGT			2600
	GCCCAGAGGT GTGCTGGTCC CCTCCTCCAC GGCATCCAGG CCTGGCTCAA TGTTCCCGTT			2660
30	GGGGTGGGGG TGTGAGGGGT TCCTACTTGC AGCCCGGTTC TCCCGAGAGA AGCTAAGGAT			2720
	CCAGGTCCTG AGGGAGGGGC CTCTCGAAGG CAGACAGACC AGAGAGGGGG GAGGAGCCCT			2780
	TGGATGGGAG GCCAGAGGCG CTTTCCGGCC ACCCCCTCCC TCCCTGCCCC CACCCTCCTT			2840
35	CCTTCATTCA AAAGTCCCAG TGGCTGCTGC CTAGGGTCCA GGCGCTGGCC GCACGCCTCC			2900
	TCGAAGCCGT TGTGCAAACA TCACTGGAGG AAGCCAGGGC TCCTCCCGGG CTGTGTATCC			2960
40	TCACTCAGGC ATCCTGTCCT CCCCAGTATC AGGAGATGTC AAGCGTCTGA AGGCTGTGTG			3020
	CCCTGGGCGT GTCTGCAAGT CACCCCAGAC ACATGTTCTC GCCATTTTAC AGATGAGAAC			3080
	ACTGAGGTTG TACTCAAGGG CACCCTGCGA GATGGAGCAA CAGCAAATA GATGGGCTTC			3140
45	TGCTGTCCTC TTGGCCAGAG GTCTCTCCAC AGGAGCCCCT GCCCCTGTAG GAAGCAGAGT			3200
	TTTAGAACAT GGAAGAAGAA GAGGGGGATG GCCCTGGACG CTGACCTCTC CCAAGCCCCC			3260
50	ACGGGGGAAA AGGCCCCCTC CTTTTCTGTC ACTCTCGGGG ACCTGCGGAG TTGAGCATTC			3320
	GTGCCCCGTG TGTCTGAAGA GTTCCCAGTG GAAAGAAGAA AAGAGGGTGT TTGTCAGTGC			3380
	CGGGGAGGGC CTGATCCCCA GACAGCTGAA GTTTAAGGTC CTTGTCCCTG TGAGCTTTAA			3440
55	CCAGCACCTC CGGGCTGACC CTTGCTAACA CATCAGAAAT GTGATTTAAT CATTAAACAT			3500
	TGTGATTGCC ACTGGGA			3517

60

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

65

(A) LENGTH: 773 amino acids

(B) TYPE: amino acid
 (C) STRANDNESS: single
 (D) TOPOLOGY: linear
 DESCRIPTION: Rabbit polyimmunoglobulin receptor

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

10	Met	Ala	Leu	Phe	Leu	Leu	Thr	Cys	Leu	Leu	Ala	Val	Phe	Ser	Ala	Ala	1	5	10	15
15	Thr	Ala	Gln	Ser	Ser	Leu	Leu	Gly	Pro	Ser	Ser	Ile	Phe	Gly	Pro	Gly	20	25	30	
20	Glu	Val	Asn	Val	Leu	Glu	Gly	Asp	Ser	Val	Ser	Ile	Thr	Cys	Tyr	Tyr	35	40	45	
25	Pro	Thr	Thr	Ser	Val	Thr	Arg	His	Ser	Arg	Lys	Phe	Trp	Cys	Arg	Glu	50	55	60	
30	Glu	Glu	Ser	Gly	Arg	Cys	Val	Thr	Leu	Ala	Ser	Thr	Gly	Tyr	Thr	Ser	65	70	75	80
35	Gln	Glu	Tyr	Ser	Gly	Arg	Gly	Lys	Leu	Thr	Asp	Phe	Pro	Asp	Lys	Gly	85	90	95	
40	Glu	Phe	Val	Val	Thr	Val	Asp	Gln	Leu	Thr	Gln	Asn	Asp	Ser	Gly	Ser	100	105	110	
45	Tyr	Lys	Cys	Gly	Val	Gly	Val	Asn	Gly	Arg	Gly	Leu	Asp	Phe	Gly	Val	115	120	125	
50	Asn	Val	Leu	Val	Ser	Gln	Lys	Pro	Glu	Pro	Asp	Asp	Val	Val	Tyr	Lys	130	135	140	
55	Gln	Tyr	Glu	Ser	Tyr	Thr	Val	Thr	Ile	Thr	Cys	Pro	Phe	Thr	Tyr	Ala	145	150	155	160
60	Thr	Arg	Gln	Leu	Lys	Lys	Ser	Phe	Tyr	Lys	Val	Glu	Asp	Gly	Glu	Leu	165	170	175	
65	Val	Leu	Ile	Ile	Asp	Ser	Ser	Ser	Lys	Glu	Ala	Lys	Asp	Pro	Arg	Tyr	180	185	190	
70	Lys	Gly	Arg	Ile	Thr	Leu	Gln	Ile	Gln	Ser	Thr	Thr	Ala	Lys	Glu	Phe	195	200	205	
75	Thr	Val	Thr	Ile	Lys	His	Leu	Gln	Leu	Asn	Asp	Ala	Gly	Gln	Tyr	Val	210	215	220	
80	Cys	Gln	Ser	Gly	Ser	Asp	Pro	Thr	Ala	Glu	Glu	Gln	Asn	Val	Asp	Leu	225	230	235	240
85	Arg	Leu	Leu	Thr	Pro	Gly	Leu	Leu	Tyr	Gly	Asn	Leu	Gly	Gly	Ser	Val	245	250	255	
90	Thr	Phe	Glu	Cys	Ala	Leu	Asp	Ser	Glu	Asp	Ala	Asn	Ala	Val	Ala	Ser	260	265	270	
95	Leu	Arg	Gln	Val	Arg	Gly	Gly	Asn	Val	Val	Ile	Asp	Ser	Gln	Gly	Thr	275	280	285	
100	Ile	Asp	Pro	Ala	Phe	Glu	Gly	Arg	Ile	Leu	Phe	Thr	Lys	Ala	Glu	Asn	290	295	300	
105	Gly	His	Phe	Ser	Val	Val	Ile	Ala	Gly	Leu	Arg	Lys	Glu	Asp	Thr	Gly	305	310	315	320

	Asn	Tyr	Leu	Cys	Gly	Val	Gln	Ser	Asn	Gly	Gln	Ser	Gly	Asp	Gly	Pro
					325					330					335	
5	Thr	Gln	Leu	Arg	Gln	Leu	Phe	Val	Asn	Glu	Glu	Ile	Asp	Val	Ser	Arg
				340					345					350		
	Ser	Pro	Pro	Val	Leu	Lys	Gly	Phe	Pro	Gly	Gly	Ser	Val	Thr	Ile	Arg
				355				360					365			
10	Cys	Pro	Tyr	Asn	Pro	Lys	Arg	Ser	Asp	Ser	His	Leu	Gln	Leu	Tyr	Leu
		370					375					380				
	Trp	Glu	Gly	Ser	Gln	Thr	Arg	His	Leu	Leu	Val	Asp	Ser	Gly	Glu	Gly
	385					390					395					400
15	Leu	Val	Gln	Lys	Asp	Tyr	Thr	Gly	Arg	Leu	Ala	Leu	Phe	Glu	Glu	Pro
					405					410					415	
	Gly	Asn	Gly	Thr	Phe	Ser	Val	Val	Leu	Asn	Gln	Leu	Thr	Ala	Glu	Asp
20				420					425					430		
	Glu	Gly	Phe	Tyr	Trp	Cys	Val	Ser	Asp	Asp	Asp	Glu	Ser	Leu	Thr	Thr
			435					440					445			
25	Ser	Val	Lys	Leu	Gln	Ile	Val	Asp	Gly	Glu	Pro	Ser	Pro	Thr	Ile	Asp
		450					455					460				
	Lys	Phe	Thr	Ala	Val	Gln	Gly	Glu	Pro	Val	Glu	Ile	Thr	Cys	His	Phe
	465					470					475					480
30	Pro	Cys	Lys	Tyr	Phe	Ser	Ser	Glu	Lys	Tyr	Trp	Cys	Lys	Trp	Asn	Asp
					485					490					495	
	His	Gly	Cys	Glu	Asp	Leu	Pro	Thr	Lys	Leu	Ser	Ser	Ser	Gly	Asp	Leu
35				500					505					510		
	Val	Lys	Cys	Asn	Asn	Asn	Leu	Val	Leu	Thr	Leu	Thr	Leu	Asp	Ser	Val
			515					520					525			
40	Ser	Glu	Asp	Asp	Glu	Gly	Trp	Tyr	Trp	Cys	Gly	Ala	Lys	Asp	Gly	His
		530					535					540				
	Glu	Phe	Glu	Glu	Val	Ala	Ala	Val	Arg	Val	Glu	Leu	Thr	Glu	Pro	Ala
	545					550					555					560
45	Lys	Val	Ala	Val	Glu	Pro	Ala	Lys	Val	Pro	Val	Asp	Pro	Ala	Lys	Ala
					565					570					575	
	Ala	Pro	Ala	Pro	Ala	Glu	Glu	Lys	Ala	Lys	Ala	Arg	Cys	Pro	Val	Pro
50				580					585					590		
	Arg	Arg	Arg	Gln	Trp	Tyr	Pro	Leu	Ser	Arg	Lys	Leu	Arg	Thr	Ser	Cys
			595					600					605			
55	Pro	Glu	Pro	Arg	Leu	Leu	Ala	Glu	Glu	Val	Ala	Val	Gln	Ser	Ala	Glu
		610					615					620				
	Asp	Pro	Ala	Ser	Gly	Ser	Arg	Ala	Ser	Val	Asp	Ala	Ser	Ser	Ala	Ser
	625					630					635					640
60	Gly	Gln	Ser	Gly	Ser	Ala	Lys	Val	Leu	Ile	Ser	Thr	Leu	Val	Pro	Leu

25 (2) INFORMATION FOR SEQ ID NO: 3:

30

(A)	LENGTH:	2919 base pairs
(B)	TYPE:	nucleic acid
(C)	STRANDEDNESS:	single
(D)	TOPOLOGY:	linear
	DESCRIPTION:	Human polyimmunoglobulin Receptor

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 235....2472

	AGAGTTTCAG	TTTTGGCAGC	AGCGTCCAGT	GCCCTGCCAG	TAGCTCCTAG	AGAGGCAGGG	60
45	GTTACCAACT	GGCCAGCAGG	CTGTGTCCCT	GAAGTCAGAT	CAACGGGAGA	GAAGGAAGTG	120
	GCTAAACAT	TGCACAGGAG	AAGTCGGCCT	GAGTGGTGCG	GCGCTCGGGA	CCCACCAGCA	180
50	ATGCTGCTCT	TCGTGCTCAC	CTGCCTGCTG	GCGGTCTTCC	CAGCCATCTC	CACG AAG Lys 1	237
	AGT CCC ATA TTT GGT CCC GAG GAG GTG AAT AGT GTG GAA GGT AAC TCA	285					
55	Ser Pro Ile Phe Gly Pro Glu Glu Val Asn Ser Val Glu Gly Asn Ser	5 10 15					
	GTG TCC ATC ACG TGC TAC TAC CCA CCC ACC TCT GTC AAC CGG CAC ACC	333					
60	Val Ser Ile Thr Cys Tyr Tyr Pro Pro Thr Ser Val Asn Arg His Thr	20 25 30					
	CGG AAG TAC TGG TGC CGG CAG GGA GCT AGA GGT GGC TGC ATA ACC CTC	381					
65	Arg Lys Tyr Trp Cys Arg Gln Gly Ala Arg Gly Gly Cys Ile Thr Leu	35 40 45					
	ATC TCC TCG GAG GGC TAC GTC TCC AGC AAA TAT GCA GGC AGG GCT AAC	429					
70	Ile Ser Ser Glu Gly Tyr Val Ser Ser Lys Tyr Ala Gly Arg Ala Asn	50 55 60 65					

	CTC	ACC	AAC	TTC	CCG	GAG	AAC	GGC	ACA	TTT	GTG	GTG	AAC	ATT	GCC	CAG	477
	Leu	Thr	Asn	Phe	Pro	Glu	Asn	Gly	Thr	Phe	Val	Val	Asn	Ile	Ala	Gln	
					70					75					80		
5	CTG	AGC	CAG	GAT	GAC	TCC	GGG	CGC	TAC	AAG	TGT	GGC	CTG	GGC	ATC	AAT	525
	Leu	Ser	Gln	Asp	Asp	Ser	Gly	Arg	Tyr	Lys	Cys	Gly	Leu	Gly	Ile	Asn	
				85					90					95			
10	AGC	CGA	GGC	CTG	TCC	TTT	GAT	GTC	AGC	CTG	GAG	GTC	AGC	CAG	GGT	CCT	573
	Ser	Arg	Gly	Leu	Ser	Phe	Asp	Val	Ser	Leu	Glu	Val	Ser	Gln	Gly	Pro	
			100					105						110			
15	GGG	CTC	CTA	AAT	GAC	ACT	AAA	GTC	TAC	ACA	GTG	GAC	CTG	GGC	AGA	ACG	621
	Gly	Leu	Leu	Asn	Asp	Thr	Lys	Val	Tyr	Thr	Val	Asp	Leu	Gly	Arg	Thr	
		115					120					125					
20	GTG	ACC	ATC	AAC	TGC	CCT	TTC	AAG	ACT	GAG	AAT	GCT	CAA	AAG	AGG	AAG	669
	Val	Thr	Ile	Asn	Cys	Pro	Phe	Lys	Thr	Glu	Asn	Ala	Gln	Lys	Arg	Lys	
	130					135					140					145	
25	TCC	TTG	TAC	AAG	CAG	ATA	GGC	CTG	TAC	CCT	GTG	CTG	GTC	ATC	GAC	TCC	717
	Ser	Leu	Tyr	Lys	Gln	Ile	Gly	Leu	Tyr	Pro	Val	Leu	Val	Ile	Asp	Ser	
					150					155					160		
30	AGT	GGT	TAT	GTG	AAT	CCC	AAC	TAT	ACA	GGA	AGA	ATA	CGC	CTT	GAT	ATT	765
	Ser	Gly	Tyr	Val	Asn	Pro	Asn	Tyr	Thr	Gly	Arg	Ile	Arg	Leu	Asp	Ile	
				165					170					175			
35	CAG	GGT	ACT	GGC	CAG	TTA	CTG	TTC	AGC	GTT	GTG	ATC	AAC	CAA	CTC	AGG	813
	Gln	Gly	Thr	Gly	Gln	Leu	Leu	Phe	Ser	Val	Val	Ile	Asn	Gln	Leu	Arg	
			180					185					190				
40	CTC	AGC	GAT	GCT	GGG	CAG	TAT	CTC	TGC	CAG	GCT	GGG	GAT	GAT	TCC	AAT	861
	Leu	Ser	Asp	Ala	Gly	Gln	Tyr	Leu	Cys	Gln	Ala	Gly	Asp	Asp	Ser	Asn	
		195					200					205					
45	AGT	AAT	AAG	AAG	AAT	GCT	GAC	CTC	CAA	GTG	CTA	AAG	CCC	GAG	CCC	GAG	909
	Ser	Asn	Lys	Lys	Asn	Ala	Asp	Leu	Gln	Val	Leu	Lys	Pro	Glu	Pro	Glu	
	210					215					220					225	
50	CTG	GTT	TAT	GAA	GAC	CTG	AGG	GGC	TCA	GTG	ACC	TTC	CAC	TGT	GCC	CTG	957
	Leu	Val	Tyr	Glu	Asp	Leu	Arg	Gly	Ser	Val	Thr	Phe	His	Cys	Ala	Leu	
				230					235						240		
55	GGC	CCT	GAG	GTG	GCA	AAC	GTG	GCC	AAA	TTT	CTG	TGC	CGA	CAG	AGC	AGT	1005
	Gly	Pro	Glu	Val	Ala	Asn	Val	Ala	Lys	Phe	Leu	Cys	Arg	Gln	Ser	Ser	
				245				250						255			
60	GGG	GAA	AAC	TGT	GAC	GTG	GTC	GTC	AAC	ACC	CTG	GGG	AAG	AGG	GCC	CCA	1053
	Gly	Glu	Asn	Cys	Asp	Val	Val	Val	Asn	Thr	Leu	Gly	Lys	Arg	Ala	Pro	
			260					265					270				
65	GCC	TTT	GAG	GGC	AGG	ATC	CTG	CTC	AAC	CCC	CAG	GAC	AAG	GAT	GGC	TCA	1101
	Ala	Phe	Glu	Gly	Arg	Ile	Leu	Leu	Asn	Pro	Gln	Asp	Lys	Asp	Gly	Ser	
		275					280					285					
70	TTC	AGT	GTG	GTG	ATC	ACA	GGC	CTG	AGG	AAG	GAG	GAT	GCA	GGG	CGC	TAC	1149
	Phe	Ser	Val	Val	Ile	Thr	Gly	Leu	Arg	Lys	Glu	Asp	Ala	Gly	Arg	Tyr	
	290					295					300					305	
75	CTG	TGT	GGA	GCC	CAT	TCG	GAT	GGT	CAG	CTG	CAG	GAA	GGC	TCG	CCT	ATC	1197
	Leu	Cys	Gly	Ala	His	Ser	Asp	Gly	Gln	Leu	Gln	Glu	Gly	Ser	Pro	Ile	
					310					315					320		
80	CAG	GCC	TGG	CAA	CTC	TTC	GTC	AAT	GAG	GAG	TCC	ACG	ATT	CCC	CGC	AGC	1245
	Gln	Ala	Trp	Gln	Leu	Phe	Val	Asn	Glu	Glu	Ser	Thr	Ile	Pro	Arg	Ser	

	325								330					335					
5	CCC Pro	ACT Thr	GTG Val 340	GTG Val	AAG Lys	GGG Gly	GTG Val	GCA Ala 345	GGA Gly	AGC Ser	TCT Ser	GTG Val	GCC Ala 350	GTG Val	CTC Leu	TGC Cys	1293		
10	CCC Pro	TAC Tyr 355	AAC Asn	CGT Arg	AAG Lys	GAA Glu	AGC Ser 360	AAA Lys	AGC Ser	ATC Ile	AAG Lys	TAC Tyr 365	TGG Trp	TGT Cys	CTC Leu	TGG Trp	1341		
15	GAA Glu 370	GGG Gly	GCC Ala	CAG Gln	AAT Asn	GGC Gly 375	CGC Arg	TGC Cys	CCC Pro	CTG Leu	CTG Leu 380	GTG Val	GAC Asp	AGC Ser	GAG Glu	GGG Gly 385	1389		
20	TGG Trp	GTT Val	AAG Lys	GCC Ala	CAG Gln 390	TAC Tyr	GAG Glu	GGC Gly	CGC Arg	CTC Leu 395	TCC Ser	CTG Leu	CTG Leu	GAG Glu	GAG Glu 400	CCA Pro	1437		
25	GGC Gly	AAC Asn	GGC Gly	ACC Thr 405	TTC Phe	ACT Thr	GTC Val	ATC Ile	CTC Leu 410	AAC Asn	CAG Gln	CTC Leu	ACC Thr	AGC Ser 415	CGG Arg	GAC Asp	1485		
30	GCC Ala	GGC Gly	TTC Phe 420	TAC Tyr	TGG Trp	TGT Cys	CTG Leu	ACC Thr 425	AAC Asn	GGC Gly	GAT Asp	ACT Thr	CTC Leu 430	TGG Trp	AGG Arg	ACC Thr	1533		
35	ACC Thr 435	GTG Val	GAG Glu	ATC Ile	AAG Lys	ATT Ile	ATC Ile 440	GAA Glu	GGA Gly	GAA Glu	CCA Pro	AAC Asn 445	CTC Leu	AAG Lys	GTA Val	CCA Pro	1581		
40	GGG Gly 450	AAT Asn	GTC Val	ACG Thr	GCT Ala	GTG Val 455	CTG Leu	GGA Gly	GAG Glu	ACT Thr 460	CTC Leu	AAG Lys	GTC Val	CCC Pro	TGT Cys	CAC His 465	1629		
45	TTT Phe	CCA Pro	TGC Cys	AAA Lys	TTC Phe 470	TCC Ser	TCG Ser	TAC Tyr	GAG Glu	AAA Lys 475	TAC Tyr	TGG Trp	TGC Cys	AAG Lys	TGG Trp 480	AAT Asn	1677		
50	AAC Asn	ACG Thr	GGC Gly	TGC Cys 485	CAG Gln	GCC Ala	CTG Leu	CCC Pro	AGC Ser 490	CAA Gln	GAC Asp	GAA Glu	GGC Gly 495	CCC Pro	AGC Ser	AAG Lys	1725		
55	GCC Ala	TTC Phe	GTG Val 500	AAC Asn	TGT Cys	GAC Asp	GAG Glu	AAC Asn 505	AGC Ser	CGG Arg	CTT Leu	GTC Val	TCC Ser 510	CTG Leu	ACC Thr	CTG Leu	1773		
60	AAC Asn 515	CTG Leu	GTG Val	ACC Thr	AGG Arg	GCT Ala	GAT Asp 520	GAG Glu	GGC Gly	TGG Trp	TAC Tyr	TGG Trp 525	TGT Cys	GGA Gly	GTG Val	AAG Lys	1821		
65	CAG Gln 530	GGC Gly	CAC His	TTC Phe	TAT Tyr	GGA Gly 535	GAG Glu	ACT Thr	GCA Ala	GCC Ala	GTC Val 540	TAT Tyr	GTG Val	GCA Ala	GTT Val	GAA Glu 545	1869		
70	GAG Glu	AGG Arg	AAG Lys	GCA Ala	GCG Ala 550	GGG Gly	TCC Ser	CGC Arg	GAT Asp	GTC Val 555	AGC Ser	CTA Leu	GCG Ala	AAG Lys	GCA Ala 560	GAC Asp	1917		
75	GCT Ala	GCT Ala	CCT Pro	GAT Asp 565	GAG Glu	AAG Lys	GTG Val	CTA Leu	GAC Asp 570	TCT Ser	GGT Gly	TTT Phe	CGG Arg	GAG Glu 575	ATT Ile	GAG Glu	1965		
80	AAC Asn	AAA Lys	GCC Ala 580	ATT Ile	CAG Gln	GAT Asp	CCC Pro	AGG Arg 585	CTT Leu	TTT Phe	GCA Ala	GAG Glu	GAA Glu 590	AAG Lys	GCG Ala	GTG Val	2013		

	GCA Ala	GAT Asp	ACA Thr	AGA Arg	GAT Asp	CAA Gln	GCC Ala	GAT Asp	GGG Gly	AGC Ser	AGA Arg	GCA Ala	TCT Ser	GTG Val	GAT Asp	TCC Ser	2061
		595					600					605					
5	GGC Gly	AGC Ser	TCT Ser	GAG Glu	GAA Glu	CAA Gln	GGT Gly	GGA Gly	AGC Ser	TCC Ser	AGA Arg	GCG Ala	CTG Leu	GTC Val	TCC Ser	ACC Thr	2109
	610					615					620					625	
10	CTG Leu	GTG Val	CCC Pro	CTG Leu	GGC Gly	CTG Leu	GTG Val	CTG Leu	GCA Ala	GTG Val	GGA Gly	GCC Ala	GTG Val	GCT Ala	GTG Val	GGG Gly	2157
					630					635					640		
15	GTG Val	GCC Ala	AGA Arg	GCC Ala	CGG Arg	CAC His	AGG Arg	AAG Lys	AAC Asn	GTC Val	GAC Asp	CGA Arg	GTT Val	TCA Ser	ATC Ile	AGA Arg	2205
				645					650					655			
	AGC Ser	TAC Tyr	AGG Arg	ACA Thr	GAC Asp	ATT Ile	AGC Ser	ATG Met	TCA Ser	GAC Asp	TTC Phe	GAG Glu	AAC Asn	TCC Ser	AGG Arg	GAA Glu	2253
			660					665					670				
20	TTT Phe	GGA Gly	GCC Ala	AAT Asn	GAC Asp	AAC Asn	ATG Met	GGA Gly	GCC Ala	TCT Ser	TCG Ser	ATC Ile	ACT Thr	CAG Gln	GAG Glu	ACA Thr	2301
		675					680					685					
25	TCC Ser	CTC Leu	GGA Gly	GGA Gly	AAA Lys	GAA Glu	GAG Glu	TTT Phe	GTT Val	GCC Ala	ACC Thr	ACT Thr	GAG Glu	AGC Ser	ACC Thr	ACA Thr	2349
		690				695					700					705	
30	GAG Glu	ACC Thr	AAA Lys	GAA Glu	CCC Pro	AAG Lys	AAG Lys	GCA Ala	AAA Lys	AGG Arg	TCA Ser	TCC Ser	AAG Lys	GAG Glu	GAA Glu	GCC Ala	2397
					710					715					720		
35	GAG Glu	ATG Met	GCC Ala	TAC Tyr	AAA Lys	GAC Asp	TTC Phe	CTG Leu	CTC Leu	CAG Gln	TCC Ser	AGC Ser	ACC Thr	GTG Val	GCC Ala	GCC Ala	2445
				725					730					735			
	GAG Glu	GCC Ala	CAG Gln	GAC Asp	GGC Gly	CCC Pro	CAG Gln	GAA Glu	GCC Ala	TAGACGGTGT CGCCGCCTGC TCCCTGCA							2500
			740				745										
40	CCCATGACAA TCACCTTCAG AATCATGTCG ATCCTGGGGG CCCTCAGCTC CTGGGGACCC 2560																
	CACTCCCTGC TCTAACACCT GCCTAGGTTT TTCCTACTGT CCTCAGAGGC GTGCTGGTCC 2620																
45	CCTCCTCAGT GACATCAAAG CCTGGCCTAA TTGTTCCTAT TGGGGATGAG GGTGGCATGA 2680																
	GGAGGTCCCA CTTGCAACTT CTTTCTGTTG AGAGAACCTC AGGTACGGAG AAGAATAGAG 2740																
	GTCCTCATGG GTCCCTTGAA GGAAGAGGGA CCAGGGTGGG AGAGCTGATT GCAGAAAGGA 2800																
50	GAGACGTGCA GCGCCCCCTCT GCACCCTTAT CATGGGATGT CAACAGAATT TTTTCCCTCC 2860																
	ACTCCATCCC TCCCTCCCGT CCTTCCCCTC TTCTTCTTTC CTTACCATCA AAAGATGTA 2919																

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

(A)	LENGTH:	746 amino acids
(B)	TYPE:	amino acid
(C)	STRANDNESS:	single
(D)	TOPOLOGY:	linear
	DESCRIPTION:	Human Polyimmunoglobulin Receptor

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4

5	Lys 1	Ser	Pro	Ile	Phe 5	Gly	Pro	Glu	Glu	Val 10	Asn	Ser	Val	Glu	Gly 15	Asn
	Ser	Val	Ser	Ile 20	Thr	Cys	Tyr	Tyr	Pro 25	Pro	Thr	Ser	Val	Asn 30	Arg	His
10	Thr	Arg	Lys 35	Tyr	Trp	Cys	Arg	Gln 40	Gly	Ala	Arg	Gly	Gly 45	Cys	Ile	Thr
	Leu	Ile 50	Ser	Ser	Glu	Gly	Tyr 55	Val	Ser	Ser	Lys	Tyr 60	Ala	Gly	Arg	Ala
15	Asn 65	Leu	Thr	Asn	Phe	Pro 70	Glu	Asn	Gly	Thr	Phe 75	Val	Val	Asn	Ile	Ala 80
	Gln	Leu	Ser	Gln	Asp 85	Asp	Ser	Gly	Arg	Tyr 90	Lys	Cys	Gly	Leu	Gly 95	Ile
20	Asn	Ser	Arg	Gly 100	Leu	Ser	Phe	Asp	Val 105	Ser	Leu	Glu	Val	Ser 110	Gln	Gly
	Pro	Gly	Leu 115	Leu	Asn	Asp	Thr	Lys 120	Val	Tyr	Thr	Val	Asp 125	Leu	Gly	Arg
25	Thr	Val 130	Thr	Ile	Asn	Cys	Pro 135	Phe	Lys	Thr	Glu	Asn 140	Ala	Gln	Lys	Arg
30	Lys 145	Ser	Leu	Tyr	Lys	Gln 150	Ile	Gly	Leu	Tyr	Pro 155	Val	Leu	Val	Ile	Asp 160
	Ser	Ser	Gly	Tyr	Val 165	Asn	Pro	Asn	Tyr	Thr 170	Gly	Arg	Ile	Arg	Leu 175	Asp
35	Ile	Gln	Gly	Thr 180	Gly	Gln	Leu	Leu	Phe 185	Ser	Val	Val	Ile	Asn 190	Gln	Leu
	Arg	Leu	Ser 195	Asp	Ala	Gly	Gln	Tyr 200	Leu	Cys	Gln	Ala	Gly 205	Asp	Asp	Ser
40	Asn	Ser 210	Asn	Lys	Lys	Asn	Ala 215	Asp	Leu	Gln	Val	Leu 220	Lys	Pro	Glu	Pro
	Glu	Leu	Val	Tyr	Glu	Asp 230	Leu	Arg	Gly	Ser	Val 235	Thr	Phe	His	Cys	Ala 240
45	Leu	Gly	Pro	Glu	Val	Ala	Asn	Val	Ala	Lys 250	Phe	Leu	Cys	Arg	Gln 255	Ser
50	Ser	Gly	Glu	Asn 260	Cys	Asp	Val	Val	Val 265	Asn	Thr	Leu	Gly	Lys 270	Arg	Ala
	Pro	Ala	Phe 275	Glu	Gly	Arg	Ile	Leu 280	Leu	Asn	Pro	Gln	Asp 285	Lys	Asp	Gly
55	Ser	Phe 290	Ser	Val	Val	Ile	Thr 295	Gly	Leu	Arg	Lys	Glu 300	Asp	Ala	Gly	Arg
60	Tyr 305	Leu	Cys	Gly	Ala	His 310	Ser	Asp	Gly	Gln	Leu 315	Gln	Glu	Gly	Ser	Pro 320
	Ile	Gln	Ala	Trp	Gln 325	Leu	Phe	Val	Asn	Glu 330	Glu	Ser	Thr	Ile	Pro 335	Arg
65	Ser	Pro	Thr	Val	Val	Lys	Gly	Val	Ala	Gly	Ser	Ser	Val	Ala	Val	Leu

			340					345					350				
		Cys	Pro	Tyr	Asn	Arg	Lys	Glu	Ser	Lys	Ser	Ile	Lys	Tyr	Trp	Cys	Leu
				355					360					365			
5		Trp	Glu	Gly	Ala	Gln	Asn	Gly	Arg	Cys	Pro	Leu	Leu	Val	Asp	Ser	Glu
			370					375					380				
10		Gly	Trp	Val	Lys	Ala	Gln	Tyr	Glu	Gly	Arg	Leu	Ser	Leu	Leu	Glu	Glu
		385					390					395					400
		Pro	Gly	Asn	Gly	Thr	Phe	Thr	Val	Ile	Leu	Asn	Gln	Leu	Thr	Ser	Arg
						405					410					415	
15		Asp	Ala	Gly	Phe	Tyr	Trp	Cys	Leu	Thr	Asn	Gly	Asp	Thr	Leu	Trp	Arg
					420					425					430		
20		Thr	Thr	Val	Glu	Ile	Lys	Ile	Ile	Glu	Gly	Glu	Pro	Asn	Leu	Lys	Val
				435					440					445			
		Pro	Gly	Asn	Val	Thr	Ala	Val	Leu	Gly	Glu	Thr	Leu	Lys	Val	Pro	Cys
			450					455					460				
25		His	Phe	Pro	Cys	Lys	Phe	Ser	Ser	Tyr	Glu	Lys	Tyr	Trp	Cys	Lys	Trp
		465					470					475					480
		Asn	Asn	Thr	Gly	Cys	Gln	Ala	Leu	Pro	Ser	Gln	Asp	Glu	Gly	Pro	Ser
						485					490					495	
30		Lys	Ala	Phe	Val	Asn	Cys	Asp	Glu	Asn	Ser	Arg	Leu	Val	Ser	Leu	Thr
					500					505					510		
		Leu	Asn	Leu	Val	Thr	Arg	Ala	Asp	Glu	Gly	Trp	Tyr	Trp	Cys	Gly	Val
				515					520					525			
35		Lys	Gln	Gly	His	Phe	Tyr	Gly	Glu	Thr	Ala	Ala	Val	Tyr	Val	Ala	Val
			530					535					540				
40		Glu	Glu	Arg	Lys	Ala	Ala	Gly	Ser	Arg	Asp	Val	Ser	Leu	Ala	Lys	Ala
		545					550					555					560
		Asp	Ala	Ala	Pro	Asp	Glu	Lys	Val	Leu	Asp	Ser	Gly	Phe	Arg	Glu	Ile
						565					570					575	
45		Glu	Asn	Lys	Ala	Ile	Gln	Asp	Pro	Arg	Leu	Phe	Ala	Glu	Glu	Lys	Ala
					580					585					590		
		Val	Ala	Asp	Thr	Arg	Asp	Gln	Ala	Asp	Gly	Ser	Arg	Ala	Ser	Val	Asp
				595					600					605			
50		Ser	Gly	Ser	Ser	Glu	Glu	Gln	Gly	Gly	Ser	Ser	Arg	Ala	Leu	Val	Ser
			610					615					620				
55		Thr	Leu	Val	Pro	Leu	Gly	Leu	Val	Leu	Ala	Val	Gly	Ala	Val	Ala	Val
		625					630					635					640
		Gly	Val	Ala	Arg	Ala	Arg	His	Arg	Lys	Asn	Val	Asp	Arg	Val	Ser	Ile
						645					650					655	
60		Arg	Ser	Tyr	Arg	Thr	Asp	Ile	Ser	Met	Ser	Asp	Phe	Glu	Asn	Ser	Arg
					660					665					670		
		Glu	Phe	Gly	Ala	Asn	Asp	Asn	Met	Gly	Ala	Ser	Ser	Ile	Thr	Gln	Glu
				675					680					685			
65		Thr	Ser	Leu	Gly	Gly	Lys	Glu	Glu	Phe	Val	Ala	Thr	Thr	Glu	Ser	Thr

40307-2042663

690 695 700

Thr Glu Thr Lys Glu Pro Lys Lys Ala Lys Arg Ser Ser Lys Glu Glu
705 710 715 720

5 Ala Glu Met Ala Tyr Lys Asp Phe Leu Leu Gln Ser Ser Thr Val Ala
725 730 735

10 Ala Glu Ala Gln Asp Gly Pro Gln Glu Ala
740 745

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3630 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
DESCRIPTION: Bovine Polyimmunoglobulin Receptor

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 152....2425

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

30 GATCTCCTCG GAGGGTCGTG CAGCGGCCCT GGGTCCCTGC CGGCACCAGT ACTTGCGCGT 60
GTGCTCCCAA AGCTGACGGG ATAGGAGGAA GGAGCTCAAA CAACCACACA GGACGGTGGC 120
35 TGGCGGCAGA GACCCGCGGG AGCCCCCAGC G ATG TCG CGC CTG TTC CTC GCC 172
Met Ser Arg Leu Phe Leu Ala
1 5
40 TGC CTG CTG GCC ATC TTC CCA GTG GTC TCC ATG AAG AGT CCC ATC TTC 220
Cys Leu Leu Ala Ile Phe Pro Val Val Ser Met Lys Ser Pro Ile Phe
10 15 20
45 GGT CCC GAG GAG GTG AGC AGC GTG GAA GGC CGC TCA GTG TCC ATC AAG 268
Gly Pro Glu Glu Val Ser Ser Val Glu Gly Arg Ser Val Ser Ile Lys
25 30 35
50 TGC TAC TAC CCG CCC ACC TCC GTC AAC CGG CAC ACG CGC AAG TAC TGG 316
Cys Tyr Tyr Pro Pro Thr Ser Val Asn Arg His Thr Arg Lys Tyr Trp
40 45 50 55
55 TGC CGG CAG GGA GCC CAG GGC CGC TGC ACG ACC CTC ATC TCC TCG GAG 364
Cys Arg Gln Gly Ala Gln Gly Arg Cys Thr Thr Leu Ile Ser Ser Glu
60 65 70
60 GGC TAC GTC TCC GAC GAC TAC GTG GGC AGA GCC AAC CTC ACC AAC TTC 412
Gly Tyr Val Ser Asp Asp Tyr Val Gly Arg Ala Asn Leu Thr Asn Phe
75 80 85
65 CCG GAG AGC GGC ACG TTT GTG GTG GAC ATC AGC CAT CTC ACC CAT AAA 460
Pro Glu Ser Gly Thr Phe Val Val Asp Ile Ser His Leu Thr His Lys
90 95 100
GAC TCA GGG CGC TAC AAG TGT GGC CTG GGC ATT AGC AGC CGT GGC CTT 508
Asp Ser Gly Arg Tyr Lys Cys Gly Leu Gly Ile Ser Ser Arg Gly Leu
105 110 115

	AAC	TTC	GAT	GTG	AGC	CTG	GAG	GTC	AGC	CAA	GAT	CCT	GCA	CAG	GCA	AGT	556
	Asn	Phe	Asp	Val	Ser	Leu	Glu	Val	Ser	Gln	Asp	Pro	Ala	Gln	Ala	Ser	
	120					125					130					135	
5	CAT	GCC	CAC	GTG	TAC	ACT	ATA	GAC	CTG	GGC	AGG	ACT	GTG	ACC	ATC	AAC	604
	His	Ala	His	Val	Tyr	Thr	Ile	Asp	Leu	Gly	Arg	Thr	Val	Thr	Ile	Asn	
					140					145					150		
10	TGC	CCT	TTC	ACG	CGT	GCG	AAT	TCT	GAG	AAG	AGA	AAA	TCC	TTG	TGC	AAG	652
	Cys	Pro	Phe	Thr	Arg	Ala	Asn	Ser	Glu	Lys	Arg	Lys	Ser	Leu	Cys	Lys	
				155					160					165			
15	AAG	ACA	ATC	CAG	GAC	TGT	TTC	CAA	GTT	GTC	GAC	TCC	ACC	GGG	TAT	GTG	700
	Lys	Thr	Ile	Gln	Asp	Cys	Phe	Gln	Val	Val	Asp	Ser	Thr	Gly	Tyr	Val	
			170					175					180				
20	AGC	AAC	AGC	TAT	AAA	GAC	AGA	GCA	CAT	ATC	AGT	ATC	CTA	GGT	ACC	AAC	748
	Ser	Asn	Ser	Tyr	Lys	Asp	Arg	Ala	His	Ile	Ser	Ile	Leu	Gly	Thr	Asn	
		185					190					195					
25	ACA	TTA	GTG	TTC	AGC	GTT	GTC	ATC	AAC	CGA	GTC	AAG	CTC	AGT	GAT	GCT	796
	Thr	Leu	Val	Phe	Ser	Val	Val	Ile	Asn	Arg	Val	Lys	Leu	Ser	Asp	Ala	
	200					205					210					215	
30	GGG	ATG	TAT	GTC	TGC	CAG	GCT	GGG	GAC	GAT	GCC	AAA	GCC	GAT	AAA	ATC	844
	Gly	Met	Tyr	Val	Cys	Gln	Ala	Gly	Asp	Asp	Ala	Lys	Ala	Asp	Lys	Ile	
					220					225					230		
35	AAC	ATT	GAC	CTC	CAG	GTG	CTG	GAG	CCT	GAG	CCT	GAG	CTG	GTT	TAT	GGA	892
	Asn	Ile	Asp	Leu	Gln	Val	Leu	Glu	Pro	Glu	Pro	Glu	Leu	Val	Tyr	Gly	
				235					240					245			
40	GAC	TTG	AGG	AGC	TCG	GTG	ACC	TTT	GAC	TGT	TCC	CTG	GGC	CCC	GAG	GTG	940
	Asp	Leu	Arg	Ser	Ser	Val	Thr	Phe	Asp	Cys	Ser	Leu	Gly	Pro	Glu	Val	
			250					255					260				
45	GCA	AAT	GTG	CCC	AAA	TTT	CTG	TGC	CAG	AAG	AAG	AAT	GGG	GGA	GCT	TGC	988
	Ala	Asn	Val	Pro	Lys	Phe	Leu	Cys	Gln	Lys	Lys	Asn	Gly	Gly	Ala	Cys	
		265					270					275					
50	AAT	GTA	GTC	ATC	AAC	ACG	TTG	GGG	AAG	AAG	GCT	CAG	GAC	TTC	CAG	GGC	1036
	Asn	Val	Val	Ile	Asn	Thr	Leu	Gly	Lys	Lys	Ala	Gln	Asp	Phe	Gln	Gly	
	280					285					290					295	
55	AGG	ATC	GTG	TCC	GTG	CCC	AAG	GAC	AAT	GGT	GTC	TTC	AGT	GTG	CAC	ATT	1084
	Arg	Ile	Val	Ser	Val	Pro	Lys	Asp	Asn	Gly	Val	Phe	Ser	Val	His	Ile	
					300					305					310		
60	ACC	AGC	CTG	AGG	AAA	GAG	GAC	GCA	GGG	CGC	TAC	GTG	TGC	GGG	GCC	CAG	1132
	Thr	Ser	Leu	Arg	Lys	Glu	Asp	Ala	Gly	Arg	Tyr	Val	Cys	Gly	Ala	Gln	
				315					320					325			
65	CCT	GAG	GGT	GAG	CCC	CAG	GAC	GGC	TGG	CCT	GTG	CAG	GCC	TGG	CAA	CTC	1180
	Pro	Glu	Gly	Glu	Pro	Gln	Asp	Gly	Trp	Pro	Val	Gln	Ala	Trp	Gln	Leu	
			330					335					340				
70	TTC	GTC	AAT	GAA	GAG	ACG	GCA	ATC	CCC	GCA	AGC	CCC	TCC	GTG	GTG	AAA	1228
	Phe	Val	Asn	Glu	Glu	Thr	Ala	Ile	Pro	Ala	Ser	Pro	Ser	Val	Val	Lys	
		345					350					355					
75	GGT	GTG	AGG	GGA	GGC	TCT	GTG	ACT	GTA	TCT	TGC	CCC	TAC	AAC	CCT	AAG	1276
	Gly	Val	Arg	Gly	Gly	Ser	Val	Thr	Val	Ser	Cys	Pro	Tyr	Asn	Pro	Lys	
	360					365					370					375	
80	GAT	GCC	AAC	AGC	GCG	AAG	TAC	TGG	TGT	CAC	TGG	GAA	GAG	GCT	CAA	AAC	1324
	Asp	Ala	Asn	Ser	Ala	Lys	Tyr	Trp	Cys	His	Trp	Glu	Glu	Ala	Gln	Asn	

	380								385				390				
5	GGC	CGC	TGC	CCG	CGG	CTG	GTG	GAG	AGC	CGG	GGG	CTG	ATG	AAG	GAG	CAG	1372
	Gly	Arg	Cys	Pro	Arg	Leu	Val	Glu	Ser	Arg	Gly	Leu	Met	Lys	Glu	Gln	
				395					400					405			
10	TAC	GAG	GGC	AGG	CTG	GTG	CTG	CTC	ACC	GAG	CCG	GGC	AAC	GGC	ACC	TAC	1420
	Tyr	Glu	Gly	Arg	Leu	Val	Leu	Leu	Thr	Glu	Pro	Gly	Asn	Gly	Thr	Tyr	
			410					415					420				
15	ACC	GTC	ATC	CTC	AAC	CAG	CTC	ACC	GAT	CAG	GAC	GCC	GGC	TTC	TAC	TGG	1468
	Thr	Val	Ile	Leu	Asn	Gln	Leu	Thr	Asp	Gln	Asp	Ala	Gly	Phe	Tyr	Trp	
		425					430					435					
20	TGC	GTG	ACC	GAC	GGC	GAC	ACG	CGC	TGG	ATC	TCC	ACA	GTG	GAG	CTC	AAG	1516
	Cys	Val	Thr	Asp	Gly	Asp	Thr	Arg	Trp	Ile	Ser	Thr	Val	Glu	Leu	Lys	
	440					445					450					455	
25	GTT	GTC	CAA	GGA	GAA	CCA	AGC	CTC	AAG	GTA	CCC	AAG	AAC	GTC	ACG	GCT	1564
	Val	Val	Gln	Gly	Glu	Pro	Ser	Leu	Lys	Val	Pro	Lys	Asn	Val	Thr	Ala	
					460					465					470		
30	TGG	CTG	GGA	GAG	CCC	TTA	AAG	CTC	TCC	TGC	CAC	TTC	CCC	TGC	AAA	TTC	1612
	Trp	Leu	Gly	Glu	Pro	Leu	Lys	Leu	Ser	Cys	His	Phe	Pro	Cys	Lys	Phe	
				475					480					485			
35	TAC	TCC	TTT	GAG	AAG	TAC	TGG	TGT	AAG	TGG	AGC	AAC	AGA	GGC	TGC	AGC	1660
	Tyr	Ser	Phe	Glu	Lys	Tyr	Trp	Cys	Lys	Trp	Ser	Asn	Arg	Gly	Cys	Ser	
			490					495					500				
40	GCC	CTG	CCC	ACC	CAG	AAC	GAC	GGC	CCC	AGC	CAG	GCC	TTT	GTG	AGC	TGC	1708
	Ala	Leu	Pro	Thr	Gln	Asn	Asp	Gly	Pro	Ser	Gln	Ala	Phe	Val	Ser	Cys	
		505					510					515					
45	GAC	CAG	AAC	AGC	CAG	GTC	GTC	TCC	CTG	AAC	CTG	GAC	ACA	GTC	ACC	AAG	1756
	Asp	Gln	Asn	Ser	Gln	Val	Val	Ser	Leu	Asn	Leu	Asp	Thr	Val	Thr	Lys	
	520					525					530					535	
50	GAG	GAT	GAA	GGC	TGG	TAC	TGG	TGT	GGA	GTG	AAG	GAA	GGC	CCC	CGA	TAC	1804
	Glu	Asp	Glu	Gly	Trp	Tyr	Trp	Cys	Gly	Val	Lys	Glu	Gly	Pro	Arg	Tyr	
					540					545					550		
55	GGG	GAG	ACG	GCG	GCT	GTC	TAC	GTG	GCA	GTG	GAG	AGC	AGG	GTG	AAG	GGG	1852
	Gly	Glu	Thr	Ala	Ala	Val	Tyr	Val	Ala	Val	Glu	Ser	Arg	Val	Lys	Gly	
				555					560					565			
60	TCC	CAA	GGC	GCC	AAG	CAA	GTG	AAA	GCT	GCC	CCT	GCG	GGG	GCG	GCA	ATA	1900
	Ser	Gln	Gly	Ala	Lys	Gln	Val	Lys	Ala	Ala	Pro	Ala	Gly	Ala	Ala	Ile	
			570					575					580				
65	CAG	TCG	AGG	GCC	GGG	GAG	ATC	CAG	AAC	AAA	GCC	CTT	CTG	GAC	CCC	AGC	1948
	Gln	Ser	Arg	Ala	Gly	Glu	Ile	Gln	Asn	Lys	Ala	Leu	Leu	Asp	Pro	Ser	
		585					590					595					
70	TTT	TTC	GCA	AAG	GAA	AGT	GTG	AAG	GAC	GCT	GCT	GGT	GGA	CCC	GGA	GCA	1996
	Phe	Phe	Ala	Lys	Glu	Ser	Val	Lys	Asp	Ala	Ala	Gly	Gly	Pro	Gly	Ala	
	600					605					610					615	
75	CCT	GCA	GAT	CCT	GGC	CGC	CCT	ACA	GGA	TAC	AGC	GGG	AGC	TCC	AAA	GCA	2044
	Pro	Ala	Asp	Pro	Gly	Arg	Pro	Thr	Gly	Tyr	Ser	Gly	Ser	Ser	Lys	Ala	
					620					625					630		
80	CTG	GTC	TCC	ACC	CTG	GTG	CCC	CTG	GCC	CTG	GTC	CTG	GTC	GCA	GGG	GTC	2092
	Leu	Val	Ser	Thr	Leu	Val	Pro	Leu	Ala	Leu	Val	Leu	Val	Ala	Gly	Val	
				635					640					645			

	GTG	GCG	ATC	GGG	GTG	GTC	CGA	GCC	CGG	CAC	AGG	AAG	AAC	GTC	GAC	CGG	2140
	Val	Ala	Ile	Gly	Val	Val	Arg	Ala	Arg	His	Arg	Lys	Asn	Val	Asp	Arg	
			650					655					660				
5	ATT	TCA	ATC	AGG	AGC	TAC	CGG	ACA	GAT	ATC	AGC	ATG	TCA	GAC	TTT	GAG	2188
	Ile	Ser	Ile	Arg	Ser	Tyr	Arg	Thr	Asp	Ile	Ser	Met	Ser	Asp	Phe	Glu	
		665					670					675					
10	AAC	TCC	AGG	GAT	TTT	GAA	GGA	CGT	GAC	AAC	ATG	GGA	GCC	TCT	CCA	GAG	2236
	Asn	Ser	Arg	Asp	Phe	Glu	Gly	Arg	Asp	Asn	Met	Gly	Ala	Ser	Pro	Glu	
		680				685					690					695	
15	GCC	CAA	GAG	ACG	TCT	CTC	GGA	GGG	AAG	GAC	GAG	TTT	GCC	ACC	ACT	ACC	2284
	Ala	Gln	Glu	Thr	Ser	Leu	Gly	Gly	Lys	Asp	Glu	Phe	Ala	Thr	Thr	Thr	
					700					705					710		
20	GAG	GAC	ACC	GTG	GAG	AGC	AAA	GAA	CCC	AAG	AAG	GCA	AAG	AGG	TCG	TCC	2332
	Glu	Asp	Thr	Val	Glu	Ser	Lys	Glu	Pro	Lys	Lys	Ala	Lys	Arg	Ser	Ser	
				715					720					725			
25	AAG	GAG	GAA	GCC	GAC	GAG	GCC	TTC	ACC	ACC	TTC	CTC	CTC	CAG	GCC	AAA	2380
	Lys	Glu	Glu	Ala	Asp	Glu	Ala	Phe	Thr	Thr	Phe	Leu	Leu	Gln	Ala	Lys	
			730				735						740				
30	AAC	CTG	GCC	TCC	GCC	GCA	ACC	CAG	AAC	GGC	CCG	ACA	GAA	GCC	TAG	ACGGAG	2431
	Asn	Leu	Ala	Ser	Ala	Ala	Thr	Gln	Asn	Gly	Pro	Thr	Glu	Ala			
		745					750					755					
35	CCCTGGGCGC	CCCTTCCCTC	CGCACGTGGC	AATCACGCTC	CGAATCACGC	TGATCCTCAG											2491
	GGCCCTCAGC	TCGGGGGGGCT	CCACTGCCTG	CACTCACACC	CCGCCTAGGC	TTCTCCTGTC											2551
	TGTCCTCAGA	GGGTGTGCTG	GTTCTTTCTT	GGTGGCATCC	AAGCCTGGCT	TACTTGTTCC											2611
40	TATTGGGGGT	GAGGTGGTAC	GAGGAGTTCC	CACCTGCAGC	TTATTCGAAC	GAGAGAACTA											2671
	AAGGTGTGGA	GGAGAATTAA	GATCGCAGAG	GGGCCTCTCA	GAAAGAAAAG	GAGTGGGTGG											2731
	GGAGACAACC	GCAGAAAGGG	GGCCATTCAG	CGCTTCCCTG	TCCCCCTTATT	TGGGGATGTC											2791
45	AGTGGAAATCC	TCCCTTCCAC	CCCATCTCTG	CACCTCTCCA	TCCCCACTCC	ATTCCATCTT											2851
	CTCTTCTTCT	TTCCCTCATT	AAAAATGTGC	ATTTGGTTAC	TCTACTAGATT	CCAGGGACTC											2911
50	TGCTAGACAC	TGGGATAGGT	AGGCCGCAAT	CCCAGGCGGC	AGCCTTCCGC	AAACATCAAG											2971
	GAGCCCCTGG	AGCCCACAGC	ATCTCTTCAC	GTGTACACTC	ACTGACCTCT	GCCTCTGCTG											3031
	GGAGAAATCA	TAAAGGGTCT	GCAGCCCTGA	GGCCTTAGGG	ATTATGTAAC	ACAGGCATAC											3091
55	ACACAAGGCA	CCATCAACAC	ATTCTTACCA	TTTCACAGGT	GAGAAAGCCG	AGGTCCTGAG											3151
	AGGTGGAGAG	GTTTGCTCAG	AGTCAGCAAG	TGAGATGTAC	GAGTCTCAAG	CTAAAGATTT											3211
60	GACACCTGCT	GTCCCTACAG	GAGGGCCTCC	TCTCTCCAGA	TGAGACAGCA	TTCCATAGGA											3271
	AGGAGAAGAA	AAATGTAAAT	AAGACTGGTC	TTTCACAGGC	CCCACATCAG	GGAAGATAACC											3331
	CCTTTCCCTG	TCTGTCACTC	ACAGAGACCT	AATAGGATAA	GAGAATGGTC	AACACTCAAA											3391
65	CCCCCGAATG	TGAAGAGTTC	TAAGTGGAAG	GGGAGGAAAA	AGGGGGGATT	TGATGGTGCC											3451
	AGGGAGGGGC	TGATCTCCAA	AGAACTAAGG	TTTAAGTTTT	TTTGTTTTTT	TTTTTCCTTC											3511
	TTCTAAGCTC	TGCACTTCAA	CTAGCATCTA	TGAGCTGGCA	CTTGCTAACA	AATCAAAAAT											3571

GTGAATTAAT TAATAATTAA AGACCATGAT TTCCTCCAAA AAAAAAAAAA AAAAAAAAAA 3630

5 (2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 757 amino acids
 (B) TYPE: amino acid
 (C) STRANDNESS: single
 (D) TOPOLOGY: linear
 DESCRIPTION: Bovine Polyimmunoglobulin Receptor

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Met Ser Arg Leu Phe Leu Ala Cys Leu Leu Ala Ile Phe Pro Val Val
 1 5 10 15
 20 Ser Met Lys Ser Pro Ile Phe Gly Pro Glu Glu Val Ser Ser Val Glu
 20 25 30
 Gly Arg Ser Val Ser Ile Lys Cys Tyr Tyr Pro Pro Thr Ser Val Asn
 35 40 45
 25 Arg His Thr Arg Lys Tyr Trp Cys Arg Gln Gly Ala Gln Gly Arg Cys
 50 55 60
 Thr Thr Leu Ile Ser Ser Glu Gly Tyr Val Ser Asp Asp Tyr Val Gly
 30 65 70 75 80
 Arg Ala Asn Leu Thr Asn Phe Pro Glu Ser Gly Thr Phe Val Val Asp
 85 90 95
 35 Ile Ser His Leu Thr His Lys Asp Ser Gly Arg Tyr Lys Cys Gly Leu
 100 105 110
 Gly Ile Ser Ser Arg Gly Leu Asn Phe Asp Val Ser Leu Glu Val Ser
 115 120 125
 40 Gln Asp Pro Ala Gln Ala Ser His Ala His Val Tyr Thr Ile Asp Leu
 130 135 140
 Gly Arg Thr Val Thr Ile Asn Cys Pro Phe Thr Arg Ala Asn Ser Glu
 45 145 150 155 160
 Lys Arg Lys Ser Leu Cys Lys Lys Thr Ile Gln Asp Cys Phe Gln Val
 165 170 175
 50 Val Asp Ser Thr Gly Tyr Val Ser Asn Ser Tyr Lys Asp Arg Ala His
 180 185 190
 Ile Ser Ile Leu Gly Thr Asn Thr Leu Val Phe Ser Val Val Ile Asn
 195 200 205
 55 Arg Val Lys Leu Ser Asp Ala Gly Met Tyr Val Cys Gln Ala Gly Asp
 210 215 220
 Asp Ala Lys Ala Asp Lys Ile Asn Ile Asp Leu Gln Val Leu Glu Pro
 60 225 230 235 240
 Glu Pro Glu Leu Val Tyr Gly Asp Leu Arg Ser Ser Val Thr Phe Asp
 245 250 255
 65 Cys Ser Leu Gly Pro Glu Val Ala Asn Val Pro Lys Phe Leu Cys Gln
 260 265 270

Sequence for "423659"

Lys Lys Asn Gly Gly Ala Cys Asn Val Val Ile Asn Thr Leu Gly Lys
 275 280 285
 5 Lys Ala Gln Asp Phe Gln Gly Arg Ile Val Ser Val Pro Lys Asp Asn
 290 295 300
 Gly Val Phe Ser Val His Ile Thr Ser Leu Arg Lys Glu Asp Ala Gly
 305 310 315 320
 10 Arg Tyr Val Cys Gly Ala Gln Pro Glu Gly Glu Pro Gln Asp Gly Trp
 325 330 335
 Pro Val Gln Ala Trp Gln Leu Phe Val Asn Glu Glu Thr Ala Ile Pro
 340 345 350
 15 Ala Ser Pro Ser Val Val Lys Gly Val Arg Gly Gly Ser Val Thr Val
 355 360 365
 20 Ser Cys Pro Tyr Asn Pro Lys Asp Ala Asn Ser Ala Lys Tyr Trp Cys
 370 375 380
 His Trp Glu Glu Ala Gln Asn Gly Arg Cys Pro Arg Leu Val Glu Ser
 385 390 395 400
 25 Arg Gly Leu Met Lys Glu Gln Tyr Glu Gly Arg Leu Val Leu Leu Thr
 405 410 415
 Glu Pro Gly Asn Gly Thr Tyr Thr Val Ile Leu Asn Gln Leu Thr Asp
 420 425 430
 30 Gln Asp Ala Gly Phe Tyr Trp Cys Val Thr Asp Gly Asp Thr Arg Trp
 435 440 445
 Ile Ser Thr Val Glu Leu Lys Val Val Gln Gly Glu Pro Ser Leu Lys
 450 455 460
 Val Pro Lys Asn Val Thr Ala Trp Leu Gly Glu Pro Leu Lys Leu Ser
 465 470 475 480
 40 Cys His Phe Pro Cys Lys Phe Tyr Ser Phe Glu Lys Tyr Trp Cys Lys
 485 490 495
 Trp Ser Asn Arg Gly Cys Ser Ala Leu Pro Thr Gln Asn Asp Gly Pro
 500 505 510
 45 Ser Gln Ala Phe Val Ser Cys Asp Gln Asn Ser Gln Val Val Ser Leu
 515 520 525
 Asn Leu Asp Thr Val Thr Lys Glu Asp Glu Gly Trp Tyr Trp Cys Gly
 530 535 540
 Val Lys Glu Gly Pro Arg Tyr Gly Glu Thr Ala Ala Val Tyr Val Ala
 545 550 555 560
 55 Val Glu Ser Arg Val Lys Gly Ser Gln Gly Ala Lys Gln Val Lys Ala
 565 570 575
 Ala Pro Ala Gly Ala Ala Ile Gln Ser Arg Ala Gly Glu Ile Gln Asn
 580 585 590
 60 Lys Ala Leu Leu Asp Pro Ser Phe Phe Ala Lys Glu Ser Val Lys Asp
 595 600 605
 Ala Ala Gly Gly Pro Gly Ala Pro Ala Asp Pro Gly Arg Pro Thr Gly
 610 615 620

53
 54
 55
 56
 57
 58
 59
 60
 61
 62
 63
 64
 65
 66
 67
 68
 69
 70
 71
 72
 73
 74
 75
 76
 77
 78
 79
 80
 81
 82
 83
 84
 85
 86
 87
 88
 89
 90
 91
 92
 93
 94
 95
 96
 97
 98
 99
 100

Tyr Ser Gly Ser Ser Lys Ala Leu Val Ser Thr Leu Val Pro Leu Ala
 625 630 635 640
 5 Leu Val Leu Val Ala Gly Val Val Ala Ile Gly Val Val Arg Ala Arg
 645 650 655
 His Arg Lys Asn Val Asp Arg Ile Ser Ile Arg Ser Tyr Arg Thr Asp
 660 665 670
 10 Ile Ser Met Ser Asp Phe Glu Asn Ser Arg Asp Phe Glu Gly Arg Asp
 675 680 685
 Asn Met Gly Ala Ser Pro Glu Ala Gln Glu Thr Ser Leu Gly Gly Lys
 690 695 700
 15 Asp Glu Phe Ala Thr Thr Thr Glu Asp Thr Val Glu Ser Lys Glu Pro
 705 710 715 720
 20 Lys Lys Ala Lys Arg Ser Ser Lys Glu Glu Ala Asp Glu Ala Phe Thr
 725 730 735
 Thr Phe Leu Leu Gln Ala Lys Asn Leu Ala Ser Ala Ala Thr Gln Asn
 740 745 750
 25 Gly Pro Thr Glu Ala
 755

30

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

35

(A) LENGTH: 3095 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

40

DESCRIPTION: Mouse Polyimmunoglobulin Receptor

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
 (B) LOCATION: 85....2400

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

TCACCTGGAG AGAAGGAAGT AGCTAAAACA TTCTCATACA AGAAGCCAAC CTGAGCGGCA 60
 50 CAGCCCCCCT GGAAGCCACA AGCA ATG AGG CTC TAC TTG TTC ACG CTC TTG 111
 Met Arg Leu Tyr Leu Phe Thr Leu Leu
 1 5
 55 GTA ACT GTC TTT TCA GGG GTC TCC ACA AAA AGC CCC ATA TTT GGT CCC 159
 Val Thr Val Phe Ser Gly Val Ser Thr Lys Ser Pro Ile Phe Gly Pro
 10 15 20 25
 60 CAG GAG GTG AGT AGT ATA GAA GGC GAC TCT GTT TCC ATC ACG TGC TAC 207
 Gln Glu Val Ser Ser Ile Glu Gly Asp Ser Val Ser Ile Thr Cys Tyr
 30 35 40
 TAC CCA GAC ACC TCT GTC AAC CGG CAC ACC CGG AAA TAC TGG TGC CGA 255
 Tyr Pro Asp Thr Ser Val Asn Arg His Thr Arg Lys Tyr Trp Cys Arg
 45 50 55
 65

FOR THE "40T20560"

	CAA GGA GCC AGC GGC ATG TGC ACA ACG CTC ATC TCT TCA AAT GGC TAC	303
	Gln Gly Ala Ser Gly Met Cys Thr Thr Leu Ile Ser Ser Asn Gly Tyr	
	60 65 70	
5	CTC TCC AAG GAG TAT TCA GGC AGA GCC AAC CTC ATC AAC TTC CCA GAG	351
	Leu Ser Lys Glu Tyr Ser Gly Arg Ala Asn Leu Ile Asn Phe Pro Glu	
	75 80 85	
10	AAC AAC ACA TTT GTG ATT AAC ATT GAG CAG CTC ACC CAG GAC GAC ACT	399
	Asn Asn Thr Phe Val Ile Asn Ile Glu Gln Leu Thr Gln Asp Asp Thr	
	90 95 100 105	
15	GGG AGC TAC AAG TGT GGC CTG GGT ACC AGT AAC CGA GGC CTG TCC TTC	447
	Gly Ser Tyr Lys Cys Gly Leu Gly Thr Ser Asn Arg Gly Leu Ser Phe	
	110 115 120	
20	GAT GTC AGC CTG GAG GTC AGC CAG GTT CCT GAG TTG CCG AGT GAC ACC	495
	Asp Val Ser Leu Glu Val Ser Gln Val Pro Glu Leu Pro Ser Asp Thr	
	125 130 135	
25	CAC GTC TAC ACA AAG GAC ATA GGC AGA AAT GTG ACC ATT GAA TGC CCT	543
	His Val Tyr Thr Lys Asp Ile Gly Arg Asn Val Thr Ile Glu Cys Pro	
	140 145 150	
30	TTC AAA AGG GAG AAT GTT CCC AGC AAG AAA TCC CTG TGT AAG AAG ACA	591
	Phe Lys Arg Glu Asn Val Pro Ser Lys Lys Ser Leu Cys Lys Lys Thr	
	155 160 165	
35	AAC CAG TCC TGC GAA CTT GTC ATT GAC TCT ACT GAG AAG GTG AAC CCC	639
	Asn Gln Ser Cys Glu Leu Val Ile Asp Ser Thr Glu Lys Val Asn Pro	
	170 175 180 185	
40	AGC TAT ATA GGC AGA GCA AAA CTT TTT ATG AAA GGG ACC GAC CTA ACT	687
	Ser Tyr Ile Gly Arg Ala Lys Leu Phe Met Lys Gly Thr Asp Leu Thr	
	190 195 200	
45	GTA TTC TAT GTC AAC ATT AGT CAC CTA ACG CAC AAT GAT GCT GGG CTG	735
	Val Phe Tyr Val Asn Ile Ser His Leu Thr His Asn Asp Ala Gly Leu	
	205 210 215	
50	TAC ATC TGC CAA GCT GGA GAA GGT CCT AGT GCT GAT AAG AAG AAT GTT	783
	Tyr Ile Cys Gln Ala Gly Glu Gly Pro Ser Ala Asp Lys Lys Asn Val	
	220 225 230	
55	GAC CTC CAG GTG CTA GCG CCT GAG CCA GAG CTG CTT TAT AAA GAC CTG	831
	Asp Leu Gln Val Leu Ala Pro Glu Pro Glu Leu Leu Tyr Lys Asp Leu	
	235 240 245	
60	AGG TCC TCA GTG ACT TTT GAA TGT GAC CTG GGC CGT GAG GTG GCA AAC	879
	Arg Ser Ser Val Thr Phe Glu Cys Asp Leu Gly Arg Glu Val Ala Asn	
	250 255 260 265	
65	GAG GCC AAA TAT CTG TGC CGG ATG AAT AAG GAA ACC TGT GAT GTG ATC	927
	Glu Ala Lys Tyr Leu Cys Arg Met Asn Lys Glu Thr Cys Asp Val Ile	
	270 275 280	
70	ATT AAC ACC CTG GGG AAG AGG GAT CCA GAC TTT GAG GGC AGG ATC CTG	975
	Ile Asn Thr Leu Gly Lys Arg Asp Pro Asp Phe Glu Gly Arg Ile Leu	
	285 290 295	
75	ATA ACC CCC AAG GAT GAC AAT GGC CGC TTC AGT GTG TTG ATC ACA GGC	1023
	Ile Thr Pro Lys Asp Asp Asn Gly Arg Phe Ser Val Leu Ile Thr Gly	
	300 305 310	
80	CTG AGG AAG GAG GAT GCA GGG CAC TAC CAG TGT GGA GCC CAC AGT TCT	1071
	Leu Arg Lys Glu Asp Ala Gly His Tyr Gln Cys Gly Ala His Ser Ser	

	315	320	325	
5	GGT TTG CCT CAA GAA GGC TGG CCC ATC CAG ACT TGG CAA CTC TTT GTC Gly Leu Pro Gln Glu Gly Trp Pro Ile Gln Thr Trp Gln Leu Phe Val 330 335 340 345			1119
10	AAT GAA GAG TCT ACC ATT CCC AAT CGT CGC TCT GTT GTG AAG GGA GTC Asn Glu Glu Ser Thr Ile Pro Asn Arg Arg Ser Val Val Lys Gly Val 350 355 360			1167
15	ACA GGA GGC TCT GTG GCC ATC GCC TGT CCC TAT AAC CCC AAG GAA AGC Thr Gly Gly Ser Val Ala Ile Ala Cys Pro Tyr Asn Pro Lys Glu Ser 365 370 375			1215
20	AGC AGC CTC AAG TAC TGG TGT CGC TGG GAA GGG GAC GGA AAT GGA CAT Ser Ser Leu Lys Tyr Trp Cys Arg Trp Glu Gly Asp Gly Asn Gly His 380 385 390			1263
25	TGC CCC GCG CTT GTG GGG ACC CAG GCC CAG GTG CAA GAA GAG TAT GAA Cys Pro Ala Leu Val Gly Thr Gln Ala Gln Val Gln Glu Glu Tyr Glu 395 400 405			1311
30	GGC CGA CTG GCA CTG TTT GAT CAG CCA GGC AAT GGT ACT TAC ACT GTC Gly Arg Leu Ala Leu Phe Asp Gln Pro Gly Asn Gly Thr Tyr Thr Val 410 415 420 425			1359
35	ATC CTC AAC CAG CTC ACC ACC GAG GAT GCT GGC TTC TAT TGG TGT CTT Ile Leu Asn Gln Leu Thr Thr Glu Asp Ala Gly Phe Tyr Trp Cys Leu 430 435 440			1407
40	ACC AAT GGT GAC TCT CGC TGG AGA ACC ACA ATA GAA CTC CAG GTT GCC Thr Asn Gly Asp Ser Arg Trp Arg Thr Thr Ile Glu Leu Gln Val Ala 445 450 455			1455
45	GAA GCT ACA AGG GAG CCA AAC CTT GAG GTG ACG CCA CAG AAC GCA ACA Glu Ala Thr Arg Glu Pro Asn Leu Glu Val Thr Pro Gln Asn Ala Thr 460 465 470			1503
50	GCA GTA CTA GGA GAG ACC TTC ACC GTT TCC TGC CAC TAT CCG TGC AAA Ala Val Leu Gly Glu Thr Phe Thr Val Ser Cys His Tyr Pro Cys Lys 475 480 485			1551
55	TTC TAC TCC CAG GAG AAA TAC TGG TGC AAG TGG AGC AAC AAG GGT TGC Phe Tyr Ser Gln Glu Lys Tyr Trp Cys Lys Trp Ser Asn Lys Gly Cys 490 495 500 505			1599
60	CAC ATC CTG CCA AGC CAT GAC GAA GGT GCC CGC CAA TCT TCT GTG AGC His Ile Leu Pro Ser His Asp Glu Gly Ala Arg Gln Ser Ser Val Ser 510 515 520			1647
65	TGC GAC CAG AGC AGC CAG CTG GTC TCC ATG ACC CTG AAC CCG GTC AGT Cys Asp Gln Ser Ser Gln Leu Val Ser Met Thr Leu Asn Pro Val Ser 525 530 535			1695
70	AAG GAA GAT GAA GGC TGG TAC TGG TGT GGG GTA AAG CAA GGC CAG ACC Lys Glu Asp Glu Gly Trp Tyr Trp Cys Gly Val Lys Gln Gly Gln Thr 540 545 550			1743
75	TAT GGA GAA ACT ACC GCC ATC TAT ATA GCA GTT GAA GAG AGG ACC AGA Tyr Gly Glu Thr Thr Ala Ile Tyr Ile Ala Val Glu Glu Arg Thr Arg 555 560 565			1791
80	GGG TCA TCC CAT GTC AAC CCA ACA GAT GCA AAT GCA CGT GCC AAA GTC Gly Ser Ser His Val Asn Pro Thr Asp Ala Asn Ala Arg Ala Lys Val 570 575 580 585			1839

4043060

	GCT	CTG	GAA	GAA	GAG	GTA	GTG	GAC	TCC	TCC	ATC	AGT	GAA	AAA	GAG	AAC	1887
	Ala	Leu	Glu	Glu	Glu	Val	Val	Asp	Ser	Ser	Ile	Ser	Glu	Lys	Glu	Asn	
					590					595					600		
5	AAA	GCC	ATT	CCA	AAT	CCC	GGG	CCT	TTT	GCC	AAC	GAA	AGA	GAG	ATA	CAG	1935
	Lys	Ala	Ile	Pro	Asn	Pro	Gly	Pro	Phe	Ala	Asn	Glu	Arg	Glu	Ile	Gln	
				605					610					615			
10	AAT	GTG	AGA	GAC	CAA	GCT	CAG	GAG	AAC	AGA	GCA	TCT	GGG	GAT	GCT	GGC	1983
	Asn	Val	Arg	Asp	Gln	Ala	Gln	Glu	Asn	Arg	Ala	Ser	Gly	Asp	Ala	Gly	
			620				625						630				
15	AGT	GCT	GAT	GGA	CAA	AGC	AGG	AGC	TCC	AGC	TCC	AAA	GTG	CTG	TTC	TCC	2031
	Ser	Ala	Asp	Gly	Gln	Ser	Arg	Ser	Ser	Ser	Ser	Lys	Val	Leu	Phe	Ser	
		635					640					645					
20	ACC	CTG	GTG	CCC	CTG	GGT	CTG	GTG	CTG	GCA	GTG	GGT	GCT	ATA	GCT	GTG	2079
	Thr	Leu	Val	Pro	Leu	Gly	Leu	Val	Leu	Ala	Val	Gly	Ala	Ile	Ala	Val	
		650				655					660					665	
	TGG	GTG	GCC	AGA	GTC	CGA	CAT	CGG	AAG	AAT	GTA	GAC	CGC	ATG	TCA	ATC	2127
	Trp	Val	Ala	Arg	Val	Arg	His	Arg	Lys	Asn	Val	Asp	Arg	Met	Ser	Ile	
					670					675					680		
25	AGC	AGC	TAC	AGG	ACA	GAC	ATT	AGC	ATG	GCA	GAC	TTC	AAG	AAC	TCC	AGA	2175
	Ser	Ser	Tyr	Arg	Thr	Asp	Ile	Ser	Met	Ala	Asp	Phe	Lys	Asn	Ser	Arg	
				685					690					695			
30	GAT	TTG	GGA	GGC	AAT	GAC	AAC	ATG	GGG	GCC	TCT	CCA	GAC	ACA	CAG	CAA	2223
	Asp	Leu	Gly	Gly	Asn	Asp	Asn	Met	Gly	Ala	Ser	Pro	Asp	Thr	Gln	Gln	
			700					705					710				
35	ACA	GTC	ATC	GAA	GGA	AAA	GAT	GAA	ATC	GTG	ACT	ACC	ACG	GAG	TGC	ACC	2271
	Thr	Val	Ile	Glu	Gly	Lys	Asp	Glu	Ile	Val	Thr	Thr	Thr	Glu	Cys	Thr	
		715					720					725					
40	GCT	GAG	CCA	GAA	GAA	TCC	AAG	AAA	GCA	AAA	AGG	TCA	TCC	AAG	GAG	GAA	2319
	Ala	Glu	Pro	Glu	Glu	Ser	Lys	Lys	Ala	Lys	Arg	Ser	Ser	Lys	Glu	Glu	
		730				735					740					745	
	GCT	GAC	ATG	GCC	TAC	TCG	GCA	TTC	CTG	CTT	CAG	TCC	AGC	ACC	ATA	GCT	2367
	Ala	Asp	Met	Ala	Tyr	Ser	Ala	Phe	Leu	Leu	Gln	Ser	Ser	Thr	Ile	Ala	
					750					755					760		
45	GCA	CAG	GTC	CAC	GAT	GGT	CCC	CAG	GAA	GCC	TAG	GCAGTGCTGA CCACCCACCC				2420	
	Ala	Gln	Val	His	Asp	Gly	Pro	Gln	Glu	Ala							
				765				770									
50	TTGCCTGTGA CAATCAACTT GAGAATCACA CTGATCCGCT CGCAGCCCAC ACTCACCCAT																2480
	CACCTCCGCT CTTCCCTCCT GTCCTCAGAG GTGTGCTGGT TCCTTCCTCG GCCATGGAAG																2540
	CCTGGCCTAG TTACGCCTGT TTAGGAGAGA GTGTGAGGCG TTCTTTTCTC TATGAAGAGA																2600
55	GTGAGGTGGA AATGAGGAGG AGGTGAACCT GAGAGACATC TCTGGAGGAA GAGGGTTGAG																2660
	AATAGGGGCT CGTTTCAGGA GAAAAGGCCA TTTGAATCTT CTTTATAACC ATATGATAGG																2720
	ATGTCAGCGT AACTCTTCTC TCCTCCATCT CTCCTTTCCT ATCCTCTTGA TTCAAACAAC																2780
60	ACATCTGAGA ACTACTAGG CTTCAGTGCC TACTAAATGC TGAGAGCCAG GCCACAATCT																2840
	TTCTATAAAT ATTACTGGAA GAGATGCCAT CTCCTCCCAG ATTCTGTCTT TTCATTAAGA																2900
65	TAAGACATCA TTACCAGGCA TACCTCCTGC CTCTGTGCCT CATAGGCATA CACAAGCCAT																2960

AAGGGCATCA TGATTTTCAG ATGAGAAGAG ATGTTTCTCA AGAGTGCCTA GTGAGATAGA 3020
 CTAGCGTCAA ACCAGATGTG GCAACTCCTG GCTCTTGGCC TACGATCTGT CTTCAAGAAA 3080
 5 AAAAAAAAAA AAAAA 3095

10 (2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 771 amino acids
 (B) TYPE: amino acid
 (C) STRANDNESS: single
 (D) TOPOLOGY: linear
 DESCRIPTION: Mouse Polyimmunoglobulin Receptor

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Met Arg Leu Tyr Leu Phe Thr Leu Leu Val Thr Val Phe Ser Gly Val
 1 5 10 15
 Ser Thr Lys Ser Pro Ile Phe Gly Pro Gln Glu Val Ser Ser Ile Glu
 25 20 25 30
 Gly Asp Ser Val Ser Ile Thr Cys Tyr Tyr Pro Asp Thr Ser Val Asn
 35 35 40 45
 Arg His Thr Arg Lys Tyr Trp Cys Arg Gln Gly Ala Ser Gly Met Cys
 50 55 60
 Thr Thr Leu Ile Ser Ser Asn Gly Tyr Leu Ser Lys Glu Tyr Ser Gly
 65 70 75 80
 Arg Ala Asn Leu Ile Asn Phe Pro Glu Asn Asn Thr Phe Val Ile Asn
 85 90 95
 Ile Glu Gln Leu Thr Gln Asp Asp Thr Gly Ser Tyr Lys Cys Gly Leu
 100 105 110
 Gly Thr Ser Asn Arg Gly Leu Ser Phe Asp Val Ser Leu Glu Val Ser
 115 120 125
 Gln Val Pro Glu Leu Pro Ser Asp Thr His Val Tyr Thr Lys Asp Ile
 130 135 140
 Gly Arg Asn Val Thr Ile Glu Cys Pro Phe Lys Arg Glu Asn Val Pro
 145 150 155 160
 Ser Lys Lys Ser Leu Cys Lys Lys Thr Asn Gln Ser Cys Glu Leu Val
 165 170 175
 Ile Asp Ser Thr Glu Lys Val Asn Pro Ser Tyr Ile Gly Arg Ala Lys
 180 185 190
 Leu Phe Met Lys Gly Thr Asp Leu Thr Val Phe Tyr Val Asn Ile Ser
 195 200 205
 His Leu Thr His Asn Asp Ala Gly Leu Tyr Ile Cys Gln Ala Gly Glu
 210 215 220
 Gly Pro Ser Ala Asp Lys Lys Asn Val Asp Leu Gln Val Leu Ala Pro
 225 230 235 240
 Glu Pro Glu Leu Leu Tyr Lys Asp Leu Arg Ser Ser Val Thr Phe Glu

204222660

	245	250	255
5	Cys Asp Leu Gly Arg Glu Val Ala Asn Glu Ala Lys Tyr Leu Cys Arg 260 265 270		
	Met Asn Lys Glu Thr Cys Asp Val Ile Ile Asn Thr Leu Gly Lys Arg 275 280 285		
10	Asp Pro Asp Phe Glu Gly Arg Ile Leu Ile Thr Pro Lys Asp Asp Asn 290 295 300		
	Gly Arg Phe Ser Val Leu Ile Thr Gly Leu Arg Lys Glu Asp Ala Gly 305 310 315 320		
15	His Tyr Gln Cys Gly Ala His Ser Ser Gly Leu Pro Gln Glu Gly Trp 325 330 335		
	Pro Ile Gln Thr Trp Gln Leu Phe Val Asn Glu Glu Ser Thr Ile Pro 340 345 350		
20	Asn Arg Arg Ser Val Val Lys Gly Val Thr Gly Gly Ser Val Ala Ile 355 360 365		
25	Ala Cys Pro Tyr Asn Pro Lys Glu Ser Ser Ser Leu Lys Tyr Trp Cys 370 375 380		
	Arg Trp Glu Gly Asp Gly Asn Gly His Cys Pro Ala Leu Val Gly Thr 385 390 395 400		
30	Gln Ala Gln Val Gln Glu Glu Tyr Glu Gly Arg Leu Ala Leu Phe Asp 405 410 415		
	Gln Pro Gly Asn Gly Thr Tyr Thr Val Ile Leu Asn Gln Leu Thr Thr 420 425 430		
35	Glu Asp Ala Gly Phe Tyr Trp Cys Leu Thr Asn Gly Asp Ser Arg Trp 435 440 445		
40	Arg Thr Thr Ile Glu Leu Gln Val Ala Glu Ala Thr Arg Glu Pro Asn 450 455 460		
	Leu Glu Val Thr Pro Gln Asn Ala Thr Ala Val Leu Gly Glu Thr Phe 465 470 475 480		
45	Thr Val Ser Cys His Tyr Pro Cys Lys Phe Tyr Ser Gln Glu Lys Tyr 485 490 495		
	Trp Cys Lys Trp Ser Asn Lys Gly Cys His Ile Leu Pro Ser His Asp 500 505 510		
50	Glu Gly Ala Arg Gln Ser Ser Val Ser Cys Asp Gln Ser Ser Gln Leu 515 520 525		
55	Val Ser Met Thr Leu Asn Pro Val Ser Lys Glu Asp Glu Gly Trp Tyr 530 535 540		
	Trp Cys Gly Val Lys Gln Gly Gln Thr Tyr Gly Glu Thr Thr Ala Ile 545 550 555 560		
60	Tyr Ile Ala Val Glu Glu Arg Thr Arg Gly Ser Ser His Val Asn Pro 565 570 575		
	Thr Asp Ala Asn Ala Arg Ala Lys Val Ala Leu Glu Glu Glu Val Val 580 585 590		
65	Asp Ser Ser Ile Ser Glu Lys Glu Asn Lys Ala Ile Pro Asn Pro Gly		

```

595                               600                               605
Pro Phe Ala Asn Glu Arg Glu Ile Gln Asn Val Arg Asp Gln Ala Gln
610                               615                               620
5
Glu Asn Arg Ala Ser Gly Asp Ala Gly Ser Ala Asp Gly Gln Ser Arg
625                               630                               635                               640
10
Ser Ser Ser Ser Lys Val Leu Phe Ser Thr Leu Val Pro Leu Gly Leu
645                               650                               655
Val Leu Ala Val Gly Ala Ile Ala Val Trp Val Ala Arg Val Arg His
660                               665                               670
15
Arg Lys Asn Val Asp Arg Met Ser Ile Ser Ser Tyr Arg Thr Asp Ile
675                               680                               685
Ser Met Ala Asp Phe Lys Asn Ser Arg Asp Leu Gly Gly Asn Asp Asn
690                               695                               700
20
Met Gly Ala Ser Pro Asp Thr Gln Gln Thr Val Ile Glu Gly Lys Asp
705                               710                               715                               720
Glu Ile Val Thr Thr Thr Glu Cys Thr Ala Glu Pro Glu Glu Ser Lys
725                               730                               735
25
Lys Ala Lys Arg Ser Ser Lys Glu Glu Ala Asp Met Ala Tyr Ser Ala
740                               745                               750
30
Phe Leu Leu Gln Ser Ser Thr Ile Ala Ala Gln Val His Asp Gly Pro
755                               760                               765
Gln Glu Ala
770
35
(2) INFORMATION FOR SEQ ID NO: 9:
40
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3269 base pairs
(B) TYPE: nucleic acid
45
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
DESCRIPTION: Rat Polyimmunoglobulin Receptor
(ix) FEATURE:
50
(A) NAME/KEY: Coding Sequence
(B) LOCATION: 74....2383
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
55 GGCAACGAAG GTACCATGGA TCTTATACAA GAAGTGAACC AACATGCCGC AACCTCCTTG 60
GAAGCCACAA GCG ATG AGG CTC TCC TTG TTC GCC CTC TTG GTA ACT GTC 109
Met Arg Leu Ser Leu Phe Ala Leu Leu Val Thr Val
1 5 10
60
TTC TCA GGG GTC TCC ACA CAA AGC CCC ATA TTT GGT CCC CAG GAT GTG 157
Phe Ser Gly Val Ser Thr Gln Ser Pro Ile Phe Gly Pro Gln Asp Val
15 20 25
65 AGT AGT ATT GAA GGT AAC TCG GTC TCC ATC ACG TGC TAC TAC CCA GAC 205
Ser Ser Ile Glu Gly Asn Ser Val Ser Ile Thr Cys Tyr Tyr Pro Asp

```

	30	35	40	
5	ACC TCT GTC AAC CGG CAC Thr Ser Val Asn Arg His 45 50	ACC CGG AAA TAC TGG TGC CGA CAA GGA GCC Thr Arg Lys Tyr Trp Cys Arg Gln Gly Ala 55 60	253	
10	AAC GGC TAC TGC GCA ACC CTC ATC TCT TCA AAT GGC TAC CTC TCG AAG Asn Gly Tyr Cys Ala Thr Leu Ile Ser Ser Asn Gly Tyr Leu Ser Lys 65 70 75	301		
15	GAG TAT TCA GGC AGA GCC AGC CTC ATC AAC TTC CCA GAG AAT AGC ACA Glu Tyr Ser Gly Arg Ala Ser Leu Ile Asn Phe Pro Glu Asn Ser Thr 80 85 90	349		
20	TTT GTG ATT AAC ATT GCA CAT CTC ACC CAG GAG GAC ACT GGG AGC TAC Phe Val Ile Asn Ile Ala His Leu Thr Gln Glu Asp Thr Gly Ser Tyr 95 100 105	397		
25	AAG TGT GGT CTG GGT ACC ACT AAC CGA GGC CTG TTT TTC GAT GTC AGC Lys Cys Gly Leu Gly Thr Thr Asn Arg Gly Leu Phe Phe Asp Val Ser 110 115 120	445		
30	CTG GAG GTC AGC CAG GTT CCT GAG TTC CCA AAT GAC ACC CAT GTC TAC Leu Glu Val Ser Gln Val Pro Glu Phe Pro Asn Asp Thr His Val Tyr 125 130 135 140	493		
35	ACA AAG GAC ATA GGC AGA ACT GTG ACC ATC GAA TGC CGT TTC AAA GAG Thr Lys Asp Ile Gly Arg Thr Val Thr Ile Glu Cys Arg Phe Lys Glu 145 150 155	541		
40	GGG AAT GCT CAT AGC AAG AAA TCC CTG TGT AAG AAG AGA GGA GAG GCC Gly Asn Ala His Ser Lys Lys Ser Leu Cys Lys Lys Arg Gly Glu Ala 160 165 170	589		
45	TGC GAA GTT GTC ATC GAC TCT ACT GAG TAC GTG GAC CCC AGC TAT AAG Cys Glu Val Val Ile Asp Ser Thr Glu Tyr Val Asp Pro Ser Tyr Lys 175 180 185	637		
50	GAC AGA GCA ATC CTT TTT ATG AAA GGG ACC AGC CGC GAT ATA TTC TAT Asp Arg Ala Ile Leu Phe Met Lys Gly Thr Ser Arg Asp Ile Phe Tyr 190 195 200	685		
55	GTC AAC ATT AGC CAC CTA ATA CCC AGT GAT GCT GGA CTG TAT GTT TGC Val Asn Ile Ser His Leu Ile Pro Ser Asp Ala Gly Leu Tyr Val Cys 205 210 215 220	733		
60	CAA GCT GGA GAA GGC CCC AGT GCT GAT AAA AAT AAT GCT GAC CTC CAG Gln Ala Gly Glu Gly Pro Ser Ala Asp Lys Asn Asn Ala Asp Leu Gln 225 230 235	781		
65	GTG CTA GAG CCT GAG CCA GAG CTG CTT TAT AAA GAC CTG AGG TCC TCA Val Leu Glu Pro Glu Pro Glu Leu Leu Tyr Lys Asp Leu Arg Ser Ser 240 245 250	829		
70	GTG ACT TTT GAA TGT GAC CTG GGC CGT GAA GTG GCA AAT GAT GCC AAA Val Thr Phe Glu Cys Asp Leu Gly Arg Glu Val Ala Asn Asp Ala Lys 255 260 265	877		
75	TAT CTG TGT CGG AAG AAC AAG GAA ACC TGT GAT GTC ATC ATC AAC ACC Tyr Leu Cys Arg Lys Asn Lys Glu Thr Cys Asp Val Ile Ile Asn Thr 270 275 280	925		
80	CTG GGG AAG AGA GAT CCA GCC TTT GAA GGC AGG ATC CTG CTA ACC CCC Leu Gly Lys Arg Asp Pro Ala Phe Glu Gly Arg Ile Leu Leu Thr Pro 285 290 295 300	973		

20200420 12:26:50

	AGG	GAT	GAC	AAT	GGC	CGC	TTC	AGT	GTG	TTG	ATC	ACA	GGC	CTG	AGG	AAG	1021
	Arg	Asp	Asp	Asn	Gly	Arg	Phe	Ser	Val	Leu	Ile	Thr	Gly	Leu	Arg	Lys	
					305					310					315		
5	GAG	GAT	GCA	GGG	CAC	TAC	CAG	TGT	GGA	GCG	CAC	AGT	TCT	GGT	TTG	CCT	1069
	Glu	Asp	Ala	Gly	His	Tyr	Gln	Cys	Gly	Ala	His	Ser	Ser	Gly	Leu	Pro	
				320					325					330			
10	CAA	GAA	GGC	TGG	CCC	GTC	CAG	GCT	TGG	CAA	CTC	TTT	GTC	AAT	GAA	GAG	1117
	Gln	Glu	Gly	Trp	Pro	Val	Gln	Ala	Trp	Gln	Leu	Phe	Val	Asn	Glu	Glu	
			335					340					345				
15	TCC	ACG	ATT	CCC	AAT	AGT	CGC	TCT	GTT	GTG	AAG	GGT	GTC	ACA	GGA	GGC	1165
	Ser	Thr	Ile	Pro	Asn	Ser	Arg	Ser	Val	Val	Lys	Gly	Val	Thr	Gly	Gly	
		350					355					360					
20	TCT	GTG	GCC	ATC	GTC	TGT	CCC	TAT	AAC	CCC	AAG	GAA	AGC	AGC	AGC	CTC	1213
	Ser	Val	Ala	Ile	Val	Cys	Pro	Tyr	Asn	Pro	Lys	Glu	Ser	Ser	Ser	Leu	
		365				370					375					380	
	AAG	TAC	TGG	TGT	CAC	TGG	GAA	GCC	GAC	GAG	AAT	GGA	CGC	TGC	CCG	GTG	1261
	Lys	Tyr	Trp	Cys	His	Trp	Glu	Ala	Asp	Glu	Asn	Gly	Arg	Cys	Pro	Val	
					385					390					395		
25	CTC	GTG	GGG	ACC	CAG	GCC	CTG	GTG	CAA	GAA	GGA	TAT	GAA	GGC	CGA	CTG	1309
	Leu	Val	Gly	Thr	Gln	Ala	Leu	Val	Gln	Glu	Gly	Tyr	Glu	Gly	Arg	Leu	
				400					405					410			
30	GCA	CTG	TTC	GAT	CAG	CCG	GGC	AGT	GGC	GCC	TAC	ACT	GTC	ATC	CTC	AAC	1357
	Ala	Leu	Phe	Asp	Gln	Pro	Gly	Ser	Gly	Ala	Tyr	Thr	Val	Ile	Leu	Asn	
			415					420					425				
35	CAG	CTC	ACC	ACC	CAG	GAT	TCT	GGC	TTC	TAC	TGG	TGT	CTT	ACC	GAT	GGT	1405
	Gln	Leu	Thr	Thr	Gln	Asp	Ser	Gly	Phe	Tyr	Trp	Cys	Leu	Thr	Asp	Gly	
		430					435					440					
40	GAC	TCT	CGC	TGG	AGA	ACC	ACG	ATA	GAA	CTG	CAG	GTT	GCT	GAA	GCT	ACA	1453
	Asp	Ser	Arg	Trp	Arg	Thr	Thr	Ile	Glu	Leu	Gln	Val	Ala	Glu	Ala	Thr	
		445				450					455					460	
	AAG	AAG	CCA	GAC	CTT	GAG	GTG	ACA	CCA	CAG	AAC	GCG	ACC	GCG	GTG	ATA	1501
	Lys	Lys	Pro	Asp	Leu	Glu	Val	Thr	Pro	Gln	Asn	Ala	Thr	Ala	Val	Ile	
					465					470					475		
45	GGA	GAG	ACC	TTC	ACA	ATC	TCC	TGC	CAC	TAT	CCG	TGC	AAA	TTC	TAC	TCC	1549
	Gly	Glu	Thr	Phe	Thr	Ile	Ser	Cys	His	Tyr	Pro	Cys	Lys	Phe	Tyr	Ser	
				480					485					490			
50	CAG	GAG	AAA	TAC	TGG	TGC	AAG	TGG	AGC	AAC	GAC	GGC	TGC	CAC	ATC	CTG	1597
	Gln	Glu	Lys	Tyr	Trp	Cys	Lys	Trp	Ser	Asn	Asp	Gly	Cys	His	Ile	Leu	
			495					500					505				
55	CCG	AGC	CAT	GAT	GAA	GGT	GCC	CGC	CAG	TCC	TCT	GTG	AGC	TGT	GAC	CAG	1645
	Pro	Ser	His	Asp	Glu	Gly	Ala	Arg	Gln	Ser	Ser	Val	Ser	Cys	Asp	Gln	
		510					515					520					
60	AGC	AGC	CAG	ATC	GTC	TCC	ATG	ACC	CTG	AAC	CCG	GTC	AAA	AAG	GAA	GAT	1693
	Ser	Ser	Gln	Ile	Val	Ser	Met	Thr	Leu	Asn	Pro	Val	Lys	Lys	Glu	Asp	
		525				530					535					540	
	GAA	GGC	TGG	TAC	TGG	TGT	GGG	GTA	AAA	GAA	GGT	CAG	GTC	TAT	GGA	GAA	1741
	Glu	Gly	Trp	Tyr	Trp	Cys	Gly	Val	Lys	Glu	Gly	Gln	Val	Tyr	Gly	Glu	
					545					550					555		
65	ACT	ACA	GCC	ATC	TAT	GTA	GCA	GTT	GAA	GAG	AGG	ACC	AGA	GGG	TCA	CCC	1789
	Thr	Thr	Ala	Ile	Tyr	Val	Ala	Val	Glu	Glu	Arg	Thr	Arg	Gly	Ser	Pro	

	560	565	570	
5	CAC ATC AAC CCG ACA GAT GCA AAC GCA CGT GCA AAA GAT GCT CCA GAG His Ile Asn Pro Thr Asp Ala Asn Ala Arg Ala Lys Asp Ala Pro Glu 575 580 585			1837
10	GAA GAG GCA ATG GAA TCC TCT GTC AGG GAG GAT GAA AAC AAG GCC AAT Glu Glu Ala Met Glu Ser Ser Val Arg Glu Asp Glu Asn Lys Ala Asn 590 595 600			1885
15	CTG GAC CCC AGG CTT TTT GCA GAC GAA AGA GAG ATA CAG AAT GCG GGA Leu Asp Pro Arg Leu Phe Ala Asp Glu Arg Glu Ile Gln Asn Ala Gly 605 610 615 620			1933
20	GAC CAA GCT CAG GAG AAC AGA GCA TCT GGG AAT GCT GGC AGT GCT GGT Asp Gln Ala Gln Glu Asn Arg Ala Ser Gly Asn Ala Gly Ser Ala Gly 625 630 635			1981
25	GGA CAA AGC GGG AGC TCC AAA GTC CTA TTC TCC ACC CTG GTG CCC CTG Gly Gln Ser Gly Ser Ser Lys Val Leu Phe Ser Thr Leu Val Pro Leu 640 645 650			2029
30	GGT TTG GTG CTG GCA GTG GGT GCT GTG GCT GTG TGG GTG GCC AGA GTC Gly Leu Val Leu Ala Val Gly Ala Val Ala Val Trp Val Ala Arg Val 655 660 665			2077
35	CGA CAT CGG AAG AAT GTA GAC CGC ATG TCA ATC AGC AGC TAC AGG ACA Arg His Arg Lys Asn Val Asp Arg Met Ser Ile Ser Ser Tyr Arg Thr 670 675 680			2125
40	GAC ATT AGC ATG GGA GAC TTC AGG AAC TCC AGG GAT TTG GGA GGC AAT Asp Ile Ser Met Gly Asp Phe Arg Asn Ser Arg Asp Leu Gly Gly Asn 685 690 695 700			2173
45	GAC AAC ATG GGC GCC ACT CCA GAC ACA CAA GAA ACA GTC CTC GAA GGA Asp Asn Met Gly Ala Thr Pro Asp Thr Gln Glu Thr Val Leu Glu Gly 705 710 715			2221
50	AAA GAT GAA ATA GAG ACT ACC ACC GAG TGT ACC ACC GAG CCA GAG GAA Lys Asp Glu Ile Glu Thr Thr Thr Glu Cys Thr Thr Glu Pro Glu Glu 720 725 730			2269
55	TCC AAG AAA GCA AAA AGG TCA TCC AAG GAG GAA GCT GAC ATG GCC TAC Ser Lys Lys Ala Lys Arg Ser Ser Lys Glu Glu Ala Asp Met Ala Tyr 735 740 745			2317
60	TCA GCA TTC CTG TTT CAG TCC AGC ACA ATA GCT GCG CAG GTC CAT GAT Ser Ala Phe Leu Phe Gln Ser Ser Thr Ile Ala Ala Gln Val His Asp 750 755 760			2365
65	GGT CCC CAG GAA GCC TAG GCAGTGCTGA CCACCTACCC CTGCCTGTGA CAATCAACT Gly Pro Gln Glu Ala			2422
70	TGAGAATCAC ATTGATCCAC TCGCAGCCCA CCCTCGCCCA TCACCCAGGC TCTTCCCTCC			2482
75	TGTTCTCAGA GGTGTGCTGG TTCCTCCCTC AGTCGTGGAA GCCTGGCCTA CTTATGCCTG			2542
80	TTTAGGAGAG AGCGTGAGGA GTTCTTTTGT CTGTTAAAGA GTAAGGTGGA AATGAGTTGA			2602
85	GCCCAAGAGG TGTCTCTGAG AGACGAGGGT TCAGAGCAGG GGCTCATTTT AGGAGGAAGA			2662
90	GCCATTTGAA GCCTCTTTAT ACACATATGC TAGGATGTCA GGATAGCTCT TCTCCTCCAT			2722
95	CTCTCCTTTC TTCTCTTCTT GATTCAGACA ACAGATCCGA AAACCTCACTA GGCTTCCGGT			2782

20

(i) SEQUENCE CHARACTERISTICS:

30

Met Arg Leu Ser Leu Phe Ala Leu Leu Val Thr Val Phe Ser Gly Val
1 5 10 15

40 Gly Asn Ser Val Ser Ile Thr Cys Tyr Tyr Pro Asp Thr Ser Val Asn
35 40 45

Arg His Thr Arg Lys Tyr Trp Cys Arg Gln Gly Ala Asn Gly Tyr Cys
50 55 60

45 Ala Thr Leu Ile Ser Ser Asn Gly Tyr Leu Ser Lys Glu Tyr Ser Gly
65 70 75 80

Arg Ala Ser Leu Ile Asn Phe Pro Glu Asn Ser Thr Phe Val Ile Asn
85 90 95

50 Ile Ala His Leu Thr Gln Glu Asp Thr Gly Ser Tyr Lys Cys Gly Leu
100 105 110

55 Gly Thr Thr Asn Arg Gly Leu Phe Phe Asp Val Ser Leu Glu Val Ser
115 120 125

Gln Val Pro Glu Phe Pro Asn Asp Thr His Val Tyr Thr Lys Asp Ile
130 135 140

60 Gly Arg Thr Val Thr Ile Glu Cys Arg Phe Lys Glu Gly Asn Ala His
145 150 155 160

Ser Lys Lys Ser Leu Cys Lys Lys Arg Gly Glu Ala Cys Glu Val Val
165 170 175

65 Ile Asp Ser Thr Glu Tyr Val Asp Pro Ser Tyr Lys Asp Arg Ala Ile

5.

Val Ser Met Thr Leu Asn Pro Val Lys Lys Glu Asp Glu Gly Trp Tyr
 530 535 540
 5 Trp Cys Gly Val Lys Glu Gly Gln Val Tyr Gly Glu Thr Thr Ala Ile
 545 550 555 560
 Tyr Val Ala Val Glu Glu Arg Thr Arg Gly Ser Pro His Ile Asn Pro
 565 570 575
 10 Thr Asp Ala Asn Ala Arg Ala Lys Asp Ala Pro Glu Glu Glu Ala Met
 580 585 590
 Glu Ser Ser Val Arg Glu Asp Glu Asn Lys Ala Asn Leu Asp Pro Arg
 595 600 605
 15 Leu Phe Ala Asp Glu Arg Glu Ile Gln Asn Ala Gly Asp Gln Ala Gln
 610 615 620
 Glu Asn Arg Ala Ser Gly Asn Ala Gly Ser Ala Gly Gly Gln Ser Gly
 625 630 635 640
 Ser Ser Lys Val Leu Phe Ser Thr Leu Val Pro Leu Gly Leu Val Leu
 645 650 655
 25 Ala Val Gly Ala Val Ala Val Trp Val Ala Arg Val Arg His Arg Lys
 660 665 670
 Asn Val Asp Arg Met Ser Ile Ser Ser Tyr Arg Thr Asp Ile Ser Met
 675 680 685
 30 Gly Asp Phe Arg Asn Ser Arg Asp Leu Gly Gly Asn Asp Asn Met Gly
 690 695 700
 Ala Thr Pro Asp Thr Gln Glu Thr Val Leu Glu Gly Lys Asp Glu Ile
 705 710 715 720
 Glu Thr Thr Thr Glu Cys Thr Thr Glu Pro Glu Glu Ser Lys Lys Ala
 725 730 735
 40 Lys Arg Ser Ser Lys Glu Glu Ala Asp Met Ala Tyr Ser Ala Phe Leu
 740 745 750
 Phe Gln Ser Ser Thr Ile Ala Ala Gln Val His Asp Gly Pro Gln Glu
 755 760 765
 45 Ala

50 (2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

55 (A) LENGTH: 322 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 DESCRIPTION: Guy's 13 Kappa

60 (ix) FEATURE:

(A) NAME/KEY: Coding Sequence
 (B) LOCATION: 8....320

65 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

CTCGAGC GAC ATT GTG ATG ACC CAG TCT CCA GCA ATC ATG TCT GCA TCT 49
 Asp Ile Val Met Thr Gln Ser Pro Ala Ile Met Ser Ala Ser
 1 5 10

5 CCA GGG GAG AAG GTC ACC ATA ACC TGC AGT GCC AGC TCA AGT GTA AGT 97
 Pro Gly Glu Lys Val Thr Ile Thr Cys Ser Ala Ser Ser Ser Val Ser
 15 20 25 30

10 TAC ATG CAC TGG TTC CAG CAG AAG CCA GGC ACT TCT CCC AAA CTC TGG 145
 Tyr Met His Trp Phe Gln Gln Lys Pro Gly Thr Ser Pro Lys Leu Trp
 35 40 45

15 CTT TAT AGC ACA TCC AAC CTG GCT TCT GGA GTC CCT GCT CGC TTC AGT 193
 Leu Tyr Ser Thr Ser Asn Leu Ala Ser Gly Val Pro Ala Arg Phe Ser
 50 55 60

20 GGC AGT GGA TCT GGG ACC TCT TAC TCT CTC ACA ATC AGC CGA ATG GAG 241
 Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Arg Met Glu
 65 70 75

GCT GAA GAT GCT GCC ACT TAT TAC TGC CAT CAA AGG ACT AGT TAC CCG 289
 Ala Glu Asp Ala Ala Thr Tyr Tyr Cys His Gln Arg Thr Ser Tyr Pro
 80 85 90

25 TAC ACG TTC GGA GGG GGG ACC AAG CTG GAA A TA 322
 Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile
 95 100 105

30 (2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 105 amino acids
 (B) TYPE: amino acid
 (C) STRANDNESS: single
 (D) TOPOLOGY: linear
 DESCRIPTION: Guy's 13 Kappa

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

Asp Ile Val Met Thr Gln Ser Pro Ala Ile Met Ser Ala Ser Pro Gly
 1 5 10 15

45 Glu Lys Val Thr Ile Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met
 20 25 30

His Trp Phe Gln Gln Lys Pro Gly Thr Ser Pro Lys Leu Trp Leu Tyr
 35 40 45

50 Ser Thr Ser Asn Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
 50 55 60

55 Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Arg Met Glu Ala Glu
 65 70 75 80

Asp Ala Ala Thr Tyr Tyr Cys His Gln Arg Thr Ser Tyr Pro Tyr Thr
 85 90 95

60 Phe Gly Gly Gly Thr Lys Leu Glu Ile
 100 105

65 (2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

5 (A) LENGTH: 402 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 DESCRIPTION: Guy's 13 Gamma 1

10 (ix) FEATURE:

(A) NAME/KEY: Coding Sequence
 (B) LOCATION: 7...402

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

CTCGAG ATG GAA TGG ACC TGG GTT TTT CTC TTC CTC CTG TCA GGA ACT 48
 Met Glu Trp Thr Trp Val Phe Leu Phe Leu Leu Ser Gly Thr
 1 5 10

20 GCA GGC GTC CAC TCT GGG GTC CAG CTT CAG CAG TCA GGA CCT GAC CTG 96
 Ala Gly Val His Ser Gly Val Gln Leu Gln Gln Ser Gly Pro Asp Leu
 15 20 25 30

25 GTG AAA CCT GGG GCC TCA GTG AAG ATA TCC TGC AAG GCT TCT GGA TAC 144
 Val Lys Pro Gly Ala Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr
 35 40 45

30 ACA TTC ACT GAC TAC AAC ATA CAC TGG GTG AAG CAG AGC CGT GGA AAG 192
 Thr Phe Thr Asp Tyr Asn Ile His Trp Val Lys Gln Ser Arg Gly Lys
 50 55 60

35 AGC CTT GAG TGG ATT GGA TAT ATT TAT CCT TAC AAT GGT AAT ACT TAC 240
 Ser Leu Glu Trp Ile Gly Tyr Ile Tyr Pro Tyr Asn Gly Asn Thr Tyr
 65 70 75

40 TAC AAC CAG AAG TTC AAG AAC AAG GCC ACA TTG ACT GTA GAC AAT TCC 288
 Tyr Asn Gln Lys Phe Lys Asn Lys Ala Thr Leu Thr Val Asp Asn Ser
 80 85 90

45 TCC ACC TCA GCC TAC ATG GAG CTC CGC AGC CTG ACA TCT GAG GAC TCT 336
 Ser Thr Ser Ala Tyr Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser
 95 100 105 110

50 GCA GTC TAT TAC TGT GCA ACC TAC TTT GAC TAC TGG GGC CAA GGC ACC 384
 Ala Val Tyr Tyr Cys Ala Thr Tyr Phe Asp Tyr Trp Gly Gln Gly Thr
 115 120 125

ACT CTC ACA GTC TCC TCA 402
 Thr Leu Thr Val Ser Ser
 130

55

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

60 (A) LENGTH: 132 amino acids
 (B) TYPE: amino acid
 (C) STRANDNESS: single
 (D) TOPOLOGY: linear
 DESCRIPTION: Guy's 13 Gamma 1

65

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

SECRET

(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:

```
(A)   LENGTH:           31 base pairs
(B)   TYPE:             nucleic acid
(C)   STRANDEDNESS:    single
(D)   TOPOLOGY:        linear
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

ACCAGATCTA TGGGAATGGAC CTGGGTTTTT C 31

50 (2) INFORMATION FOR SEQ ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:

```
(A)   LENGTH:           30 base pairs
(B)   TYPE:             nucleic acid
(C)   STRANDEDNESS:    single
(D)   TOPOLOGY:        linear
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

CCCAAGCTTG GTTTTGGAGA TGGTTTTCTC 30

65

(i) SEQUENCE CHARACTERISTICS:

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

15
(2) INFORMATION FOR SEQ ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

30

35 (2) INFORMATION FOR SEQ ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:

```

40      (A)    LENGTH:           30 base pairs
      (B)    TYPE:              nucleic acid
      (C)    STRANDEDNESS:      single
      (D)    TOPOLOGY:          linear

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

45 GGAAAGCTTT GTACATATGC AAGGCTTACA 30